

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2004, 22:51:30 ; Search time 20 Seconds
(without alignments)

43.286 Million cell updates/sec

Title: US-09-920-480b-1

Perfect score: 40

Sequence: 1 FLDQVAFKV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	35.0	7	2 S57274	triacylglycerol li
2	13	32.5	6	2 A20186	fatty-acid synthas
3	13	32.5	7	2 PT0569	T-cell receptor be
4	13	32.5	8	2 A28004	adipokinetic hormo
5	13	32.5	8	2 S08995	hypertrehalosemic
6	13	32.5	8	2 S10596	adipokinetic hormo
7	13	32.5	8	2 A49823	adipokinetic hormo
8	13	32.5	8	2 A44960	neuropeptide led-C
9	13	32.5	8	2 S55310	adipokinetic hormo
10	13	32.5	8	2 A58220	adipokinetic hormo
11	13	32.5	8	2 A47618	beta-galactosidase
12	13	32.5	9	2 D24180	fibrinogen beta ch
13	13	32.5	9	2 S66635	alpha-2-macroglobu
14	12	30.0	5	2 B44823	synaptosomal-assoc
15	12	30.0	7	2 A28709	phosphonacetaldel
16	12	30.0	7	2 A34818	viciilin 72K chain
17	12	30.0	7	2 C56793	platelet glycoprot
18	12	30.0	7	2 PN0649	pullulanase (EC 3.
19	12	30.0	7	2 S09066	globulin IV alpha
20	12	30.0	8	2 S08996	hypertrehalosemic
21	12	30.0	8	2 B49823	adipokinetic hormo
22	12	30.0	8	2 B44860	neuropeptide led-C
23	12	30.0	8	2 A33995	adipokinetic hormo
24	12	30.0	8	2 S11545	adipokinetic hormo
25	12	30.0	8	2 E60588	sperm-activating p
26	12	30.0	8	2 G60588	sperm-activating p
27	12	30.0	8	2 B24749	neuropeptide B - b
28	12	30.0	8	2 A23967	leucopyrokinin - M
29	12	30.0	8	2 S29272	tocopherol-binding

ALIGNMENTS

RESULT 1

S57274
triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C:Species: Psychrobacter immobilis
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C:Accession: S57274
R:Arpigny, J.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
A:Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the
A:Reference number: S57274; MUID:95359197; PMID:7632728
A:Accession: S57274
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-7 <ARP>
A:Cross-references: EMBL:X67712
C:Keywords: carboxylic ester hydrolase

Query Match 35.0%; Score 14; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DOV 5
DB 5 DOI 7

RESULT 2

A20186
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-May-2000
C:Accession: A20186
R:McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.
FEBS Lett. 160, 296-300, 1983
A:Title: Amino acid sequence around the active serine in the acyl transferase domain of
A:Reference number: A20186; MUID:83287768; PMID:6554204
A:Accession: A20186
A:Molecule type: protein
A:Residues: 1-6 <MCC>
C:Keywords: acyltransferase; coenzyme A

Query Match 32.5%; Score 13; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDQVA 6
DB 2 LGEVA 6

RESULT 3

PT0569

adipokinetic hormo
kidney and bladder
ribosomal protein
[Phe-6]-mosact - s
60K Ca binding pro
Ig heavy chain CRD
macrophage inhibit
T-cell receptor be
achatin-1 - giant
endo-1,4-beta-xyla
phosphoglycerate t
alpha-tubulin - Ch
platelet-derived g
glutathione transf
phosphotransferase
nitrate reductase

30 12 30.0 9 2 A24244
31 12 30.0 9 2 G58502
32 12 30.0 9 2 S36898
33 12 30.0 9 2 JN0027
34 12 30.0 9 2 PT0080
35 12 30.0 9 2 PT0315
36 12 30.0 9 2 A61386
37 12 30.0 9 2 PH0943
38 11 27.5 4 2 A32480
39 11 27.5 5 2 S70615
40 11 27.5 6 2 T11779
41 11 27.5 6 2 I48126
42 11 27.5 6 2 I59142
43 11 27.5 7 2 S71867
44 11 27.5 7 2 B39127
45 11 27.5 8 2 S68802

T-cell receptor beta chain V-D-J region (141-14F) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0569

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0569

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-7 <FE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 32.5%; Score 13; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DQVA 6

DB 4 DAVA 7

RESULT 4

A28004

adipokinetic hormone G - two-spotted cricket

N:Alternate names: AKH-G

C:Species: Gryllus bimaculatus (two-spotted cricket)

C:Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997

C:Accession: A28004

R:Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
 A:Reference number: A28004; MUID:88106553; PMID:3426616

A:Accession: A28004

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7

DB 1 QVNF 4

RESULT 5

S08995

hypertrehalosemic hormone I - oriental cockroach

N:Alternate names: Pea-CAH-I

C:Species: Platta orientalis (oriental cockroach)

C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C:Accession: S08995

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
 A:Reference number: S08995; MUID:90253659; PMID:2340112

A:Accession: S08995

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7

DB 1 QVNF 4

RESULT 6

S10596

adipokinetic hormone - pond skimmer

C:Species: Libellula auripennis

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C:Accession: S10596

R:Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating h
 A:Reference number: S10596; MUID:90359055; PMID:2390213

A:Accession: S10596

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7

DB 1 QVNF 4

RESULT 7

A49823

adipokinetic hormone I - American cockroach

N:Alternate names: Periplanetin CC-1

C:Species: Periplaneta americana (American cockroach)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C:Accession: A49823

R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C

Proc. Natl. Acad. Sci. U.S.A. 91, 5575-5579, 1994

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hy
 A:Reference number: A49823; MUID:84298179; PMID:6591205

A:Accession: A49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7

DB 1 QVNF 4

RESULT 8

A44960

neuropeptide Led-CC-I - Colorado potato beetle

C:Species: Lepidotarsa decemlineata (Colorado potato beetle)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: A44960

R:Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
 A;Reference number: A44960; MUID:90160053; PMID:2576128
 A;Accession: A44960
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>

C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 9
 S55310
 adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
 N;Alternate names: Psi-AKH
 C;Species: Pseudagrion inconspicuum
 C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: S55310
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: S55310
 A;Molecule type: protein
 A;Residues: 1-8 <JAN>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 10
 A58620
 adipokinetic hormone - damselfly (Ischnura senegalensis)
 C;Species: Ischnura senegalensis
 C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: A58620
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: A58620
 A;Molecule type: protein
 A;Residues: 1-8 <JAN>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 11

A47618
 beta-galactosidase (EC 3.2.1.23) lacZ - Streptococcus bovis (fragment)
 C;Species: Streptococcus bovis
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
 C;Accession: A47618
 R;Gilbert, H.J.; Hall, J.
 J. Gen. Microbiol. 133, 2285-2293, 1987

A;Title: Molecular cloning of Streptococcus bovis lactose catabolic genes.

A;Reference number: A47618

A;Accession: A47618

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 <GIL>

A;Cross-references: GB:M35285; NID:G153682; PIDN:AAA26912.1; PID:G552005

C;Keywords: glycosidase; hydrolase

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QVAF 6
 Db 4 DTVA 7

RESULT 12

D24180

fibrinogen beta chain - red guenon (fragment)

N;Contains: fibrinopeptide B

C;Species: Erythrocebus patas (red guenon, hussar)

C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996

C;Accession: D24180

R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 97, 1487-1492, 1985

A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas) uenons, and baboons.

A;Reference number: A91990; MUID:85289140; PMID:3928610

A;Accession: D24180

A;Molecule type: protein

A;Residues: 1-9 <NAK>

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 32.5%; Score 13; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QVAF 7
 Db 2 EEVLf 6

RESULT 13

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottr

FEBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain of alpha-2-macroglobulin isoform 1 from zebu cattle

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DOL>

Query Match 32.5%; Score 13; DB 2; Length 9;
 Best Local Similarity 28.6%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DQVAFV 9
| : | :
Db 2 DEFPFAL 8

RESULT 14

B44823
synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)
N/Alternate names: superprotein peptide 10A
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C/Accession: B44823
P/Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: B44823; PMID:92044785; PMID:1941090
A/Accession: B44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <LOE>
A/Experimental source: visual tissue
A/Note: sequence extracted from NCBI backbone (NCBIP:64255)
C/Keywords: membrane trafficking

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DQVA 6
| : | :
Db 1 EQMA 4

RESULT 15

A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C/Species: Bacillus cereus
C/Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C/Accession: A28709
R/Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A/Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
idue.
A/Reference number: A28709; PMID:88241058; PMID:3132206
A/Accession: A28709
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <OLS>

Query Match 30.0%; Score 12; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LDQV 5
| : | :
Db 3 IDHV 6

Search completed: February 24, 2004, 22:57:23
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2004, 22:27:49 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-920-480B-1
Perfect score: 40
Sequence: 1 FLDQVAFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	37.5	8	1	ALL2_CARMA
2	14	35.0	7	1	ALL4_CARMA
3	14	35.0	8	1	NS3_MYCTU
4	14	35.0	9	1	ALL1_CARMA
5	13	32.5	8	1	AKHG_GRYBI
6	13	32.5	8	1	AKH_LIBAU
7	13	32.5	9	1	HTFI_PERAM
8	13	32.5	9	1	FIBB_ERYPA
9	12	30.0	8	1	AKH_TABAT
10	12	30.0	8	1	ALL8_CARMA
11	12	30.0	8	1	HTF2_PERAM
12	12	30.0	8	1	LPK_LEUMA
13	12	30.0	8	1	NPMB_BOVIN
14	12	30.0	9	1	MOSF_CLYXA
15	11	27.5	4	1	ACH1_ACHFU
16	11	27.5	8	1	ALL7_CARMA
17	11	27.5	8	1	ANG2_BORJA
18	11	27.5	8	1	LCK3_LEUMA
19	11	27.5	8	1	UC26_MAZE
20	11	27.5	8	1	UPAL_HUMAN
21	11	27.5	9	1	RT33_BOVIN
22	11	27.5	9	1	UF02_MOUSE
23	11	25.0	4	1	FLRF_HIERE
24	10	25.0	4	1	FLRN_ATEL
25	10	25.0	5	1	RE32_LITRU
26	10	25.0	5	1	UC22_MAZE
27	10	25.0	6	1	LOK1_LOCOM
28	10	25.0	6	1	OVN_LEPDE
29	10	25.0	7	1	ALL3_CARMA
30	10	25.0	7	1	ALL5_CARMA
31	10	25.0	7	1	ALL5_CARMA
32	10	25.0	7	1	FARI_HELTI
33	10	25.0	7	1	FARI_MACRS

34	10	25.0	7	1	FARI_PROCL
35	10	25.0	7	1	FAR2_PROCL
36	10	25.0	7	1	PPH2_LYCES
37	10	25.0	7	1	UF03_MOUSE
38	10	25.0	8	1	ALL7_CARMA
39	10	25.0	8	1	ALL8_CARMA
40	10	25.0	8	1	ALL9_CARMA
41	10	25.0	8	1	COXG_RAT
42	10	25.0	8	1	CPD1_ENTFA
43	10	25.0	8	1	FARI_PANRE
44	10	25.0	8	1	FARI_PENMO
45	10	25.0	8	1	FAR2_MACRS

ALIGNMENTS

RESULT 1					
AL12_CARMA	STANDARD;	PRT;	8 AA.		
ID AL12_CARMA					
AC P81815;					
DT 30-MAY-2000 (Rel. 39, Created)					
DT 30-MAY-2000 (Rel. 39, Last sequence update)					
DT 30-MAY-2000 (Rel. 39, Last annotation update)					
DE Carcinustatin 12.					
OS Carcinus maenas (Common shore crab) (Green crab).					
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;					
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;					
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.					
OX NCBI_TaxID=6759;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;					
RX MEDLINE=98121193; PubMed=9461295;					
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,					
RA Thorpe A.;					
RT "Isolation and identification of multiple neuropeptides of the					
RT allatostatin superfamily in the shore crab Carcinus maenas."					
RL Eur. J. Biochem. 250:727-734 (1997).					
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.					
CC -!- SIMILARITY: Belongs to the allatostatin family.					
KW Neuropeptide; Multigene family.					
SQ SEQUENCE 8 AA; 913 MW; 672879DCB569AB7 CRC64;					
Query Match 37.5%; Score 15; DB 1; Length 8;					
Best Local Similarity 60.0%; Pred. No. 1.4e+05;					
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY 3 DQVAF 7					
Db 2 DMVAF 6					
RESULT 2					
ALL4_CARMA	STANDARD;	PRT;	7 AA.		
ID ALL4_CARMA					
AC P81807;					
DT 30-MAY-2000 (Rel. 39, Created)					
DT 30-MAY-2000 (Rel. 39, Last sequence update)					
DT 30-MAY-2000 (Rel. 39, Last annotation update)					
DE Carcinustatin 4.					
OS Carcinus maenas (Common shore crab) (Green crab).					
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;					
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;					
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.					
OX NCBI_TaxID=6759;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;					
RX MEDLINE=98121193; PubMed=9461295;					
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,					
RA Thorpe A.;					
RT "Isolation and identification of multiple neuropeptides of the					

RT allatostatin superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 35.0%; Score 14; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QVAF 7
 Db 1 DPYAF 5

RESULT 3

NS3_MYCTU
 ID NS3_MYCTU STANDARD; PRT; 8 AA.

AC P81L52;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 3 (Fragment).

OS Mycobacterium tuberculosis
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.

RC STRAIN=H37RV;
 RA Prasad H.K., Annappurna P.S.;
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -!- CAUTION: We are unable to find this protein in the translation of
 CC the genome of strain H37RV.

FT NON TER 1 1
 FT NON TER 8 8

SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;
 Query Match 35.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VAF 7
 Db 2 VAF 4

RESULT 4

AL11_CARMA
 ID AL11_CARMA STANDARD; PRT; 9 AA.

AC P818L4;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 11.

OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.

OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*."

RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.

KW Neuropeptide; Amidation; Multigene family.

FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 927 MW; 832D79CDBC46D861 CRC64;

Query Match 35.0%; Score 14; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
 Db 4 QYAF 7

RESULT 5

AKHG_GRYBI
 ID AKHG_GRYBI STANDARD; PRT; 8 AA.

AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone G (AKH-G) (RO II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Gryllus.

OX NCBI_TaxID=6999, 7007;
 RN [1]
 RP SEQUENCE.

RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;

RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 RT of a peptide with adipokinetic activity from the corpora cardiaca of
 RT the cricket *Gryllus bimaculatus*."
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]
 RP SEQUENCE.

RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;

RT "Sequence analyses of two neuropeptides of the AKH/RPCH family from
 RT the lubber grasshopper, *Romalea microptera*."
 RL Peptides 9:861-888(1988).

CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.

CC -!- SUBCELLULAR LOCATION: Secreted
 CC -!- SIMILARITY: Belongs to the AKH / RPCH family.

DR PIR; A28004; A28004.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 32.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 6

AKH_LIBAU

ID AKH_LIBAU STANDARD; PRT; 8 AA.

AC P25418;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-
 RT concentrating hormone family isolated and sequenced from a
 RT dragonfly";
 RL Biol. Chem. Hoppe-Seyler 371:475-483 (1990).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; S10596; S10596.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
 Query Match 32.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVAF 7
 Db ||| 1 QVNF 4
 RESULT 7
 HTFL_PERAM STANDARD; PRT; 8 AA.
 ID HTFL_PERAM
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrichaloesamic factor I (Neuropeptide M-1) (Periplaneta CC-I)
 DE (Pea-CAR-I) (Leb-CC-I) (Hypertrichaloesamic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
 RN [3]

RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289 (1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrichaloesamic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
 CC -!- FUNCTION: Hypertrichaloesamic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is
 CC the major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A05169; A05169.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 32.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVAF 7
 Db ||| 1 QVNF 4
 RESULT 8
 FIBB_ERYPA STANDARD; PRT; 9 AA.
 ID FIBB_ERYPA
 AC P19346;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Erythrocybus patas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopitheciinae; Erythrocybus.
 OX NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
 RT patas monkey (Erythrocybus patas): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT guenons, and baboons";
 RL J. Biochem. 97:1487-1492 (1985).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,

CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.

DR PIR: D24180; D24180; Fibrinogen C.
 DR InterPro: IPR002181; Fibrinogen C.
 DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 32.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 DQVAF 7
 : : :
 Db 2 EVVLF 6

RESULT 9

AKH TABAT ID AXH TABAT STANDARD; PRT; 8 AA.
 AC P04595; (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 OS Tabanus atratus (Horse fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 CC Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE

RC TISSUE=Corpora cardiaca;
 RX MEDLINE=50046750; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR PIR; A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7
 : : :
 Db 1 QLVF 4

RESULT 10

AL18 CARMA ID AL18 CARMA STANDARD; PRT; 8 AA.
 AC P81821;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 18.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8 8 AMIDATION (POTENTIAL).
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DQVAF 7
 : : :
 Db 2 DMYSF 6

RESULT 11

HTF2 PERAM ID HTF2 PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
 DE (Pea-CAH-II) (IleD-CC-II) (Hypertrehalosemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 CC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.

RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
 RN [2]
 RP SEQUENCE.

RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
 RN [3]
 RP SEQUENCE.

RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical."
 RL Peptides 10:1287-1289 (1989).

RN [4]
 RP SEQUENCE.
 RX SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RC MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrichalosaemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blattia orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: Hypertrichalosaemic factors are neuropeptides that
 elevate the level of trehalose in the hemolymph (trehalose is the
 major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; B44960.
 DR PIR; B49823; B49823.
 DR PIR; S08996; S08996.
 DR InterPro: IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 Query Match 30.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVAF 7
 Db 1 QLTF 4
 RESULT 12
 LPK LEUMA
 ID LPK LEUMA STANDARD; PRT; 8 AA.
 AC P13049;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 28-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucopyrokinin (LPK) (LEM-PK).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86269041; PubMed=3015140;
 RA Nachman R.J., Holman G.M., Cook B.J.;
 RT "Active fragments and analogs of the insect neuropeptide
 leucopyrokinin: structure-function studies."
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
 RN [2]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of a blocked myotropic
 neuropeptide isolated from the cockroach, *Leucophaea maderae*."
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 activity).
 CC -!- MISCELLANEOUS: An analog without the N-terminal PCA residue was
 synthesized and found to exhibit greater activity (144%) than the
 parent neuropeptide. The portion of the sequence of LPK most
 critical for the myotropic properties is limited to the
 pentapeptide fragment FPPRL.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A23967; A23967.
 DR InterPro: IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
 Query Match 30.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVAF 7
 Db 1 QTSF 4
 RESULT 13
 NPMB BOVIN
 ID NPMB BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Morphine modulating neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 characterization of two brain neuropeptides that modulate the action
 of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -!- FUNCTION: Modulates the action of morphine.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 30.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLDQ 4
 Db 1 FLFQ 4
 RESULT 14
 MOSF CLYJA
 ID MOSF CLYJA STANDARD; PRT; 9 AA.
 AC P19853;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE [Phe-6]-mosact.
 OS Clypeaster japonicus (Sand dollar).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
 OC Clypeasteridae; Clypeaster.
 OX NCBI_TaxID=7644;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Egg jelly;
 RA Suzuki N., Kurita M., Yoshino K.I., Kajiuura H., Nomura K.;
 RT "Purification and structure of mosact and its derivatives from the
 egg jelly of the sea urchin *Clypeaster japonicus*."

Job time : 12 secs

RL Zool. Sci. 4:649-656(1987).
 CC -!- FUNCTION: Stimulates sperm respiration and motility.
 DR PIR; JN0027; JN0027.
 SQ SEQUENCE 9 AA; 924 MW; 93245729DC5BAB5 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AFV 9
 Db 5 AFLI 8

RESULT 15
 ACHI_ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Ferussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica ferussac containing a D-amino acid residue.";
 RN Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 [2]
 RP CHARACTERIZATION.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RN Biochem. Biophys. Res. Commun. 177:847-853(1991).
 [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=139265;
 RA Iehida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.";
 RN Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 27.5%; Score 11; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLD 3
 Db 2 FAD 4

Search completed: February 24, 2004, 22:55:58

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: February 24, 2004, 22:50:30 ; Search time 38 Seconds
(without alignments)
74.728 Million cell updates/sec

Title: US-09-920-480B-1
Perfect score: 40
Sequence: 1 FLQVAFVX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	45.0	8	2	O09258 synchococc
2	15	37.5	8	11	Q99MN0 mus musculu
3	14	35.0	7	2	O8KMS9 enterobacte
4	14	35.0	8	11	Q99NX9 hydrochoeru
5	14	35.0	9	8	Q9GD36 juncus effu
6	13	32.5	7	13	Q8JJ20 gallus gall
7	13	32.5	8	2	Q9RQ49
8	13	32.5	8	2	Q53790 streptococc
9	13	32.5	8	2	Q9RQ57
10	13	32.5	9	2	Q82568 streptococc
11	13	32.5	9	9	Q8H9Z1
12	13	32.5	9	12	Q84333
13	12	30.0	8	2	P72279
14	12	30.0	8	2	Q8GMM5
15	12	30.0	8	11	Q99MH2
16	12	30.0	8	11	Q9QVK5

17	12	30.0	9	2	Q46179	Q46179 clostridium
18	12	30.0	9	4	P78484	P78484 homo sapien
19	12	30.0	9	10	Q8LPT5	Q8LPT5 zea mays (m
20	12	30.0	9	11	Q9QWG2	Q9QWG2 mus musculu
21	11	27.5	7	5	Q7ZIC0	Q7ZIC0 caenorhabdi
22	11	27.5	7	8	Q98866	Q98866 spinacia ol
23	11	27.5	8	2	Q9R3X0	Q9R3X0 planktothri
24	11	27.5	8	4	Q9H4D3	Q9H4D3 homo sapien
25	11	27.5	8	4	Q8W8G2	Q8W8G2 diadema sav
26	11	27.5	8	8	Q8W8G4	Q8W8G4 diadema mex
27	11	27.5	8	8	Q8W8G6	Q8W8G6 diadema mex
28	11	27.5	8	8	Q8W8G5	Q8W8G5 diadema mex
29	11	27.5	8	8	Q8W8G3	Q8W8G3 diadema pau
30	11	27.5	8	8	Q8WFR5	Q8WFR5 diadema pau
31	11	27.5	9	2	Q8RKU3	Q8RKU3 borrelia bu
32	11	27.5	9	2	Q9R7H9	Q9R7H9 haemophilus
33	11	27.5	9	4	Q14715	Q14715 homo sapien
34	11	27.5	9	4	Q9BQT4	Q9BQT4 homo sapien
35	11	27.5	9	7	Q78225	Q78225 mus musculu
36	11	27.5	9	8	Q8WFT4	Q8WFT4 diadema ant
37	11	27.5	9	8	Q8WFS4	Q8WFS4 diadema mex
38	11	27.5	9	8	Q8W8X4	Q8W8X4 diadema mex
39	11	27.5	9	8	Q9MMF4	Q9MMF4 buteo rufin
40	11	27.5	9	8	Q9TLM7	Q9TLM7 laurancia v
41	11	27.5	9	8	Q9MMG9	Q9MMG9 buteo buteo
42	11	27.5	9	8	Q8W8W5	Q8W8W5 diadema set
43	11	27.5	9	8	Q8W8W6	Q8W8W6 diadema ant
44	11	27.5	9	9	Q9XTN0	Q9XTN0 bacterioph
45	11	27.5	9	10	Q9AXH8	Q9AXH8 mesembryant

ALIGNMENTS

RESULT 1
O09258 PRELIMINARY; PRT; 8 AA.
AC O09258;
DT 01-JUL-1997 (TREMREL. 04, Created)
DT 01-JUL-1997 (TREMREL. 04, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE NIFH (Fragment).
GN NIFH.
OS Synchococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synchococcus sp. strain
RT RF-1";
RL Microbiology 145:743-753 (1999).
DR EMBL; AF001780; AAC33369.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 985 NM; F16B59CDD046C406 CRC64;

Query Match 45.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 QVAF 7
Db 3 QIAP 6

RESULT 2
Q99MN0 PRELIMINARY; PRT; 8 AA.
ID Q99MN0
AC Q99MN0;
DT 01-JUN-2001 (TREMREL. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adenosine deaminase tRNA-specific 1 (Fragment).
 GN ADAT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA MEDLINE=21231131; PubMed=11331948;
 RX Maas S., Kim Y.G., Rich A.;
 RA "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
 RT tRNA synthetases.";
 RL Mamm. Genome 12:387-393 (2001).
 DR EMBL; AF328904; AAK19310.1; -.
 DR MGD; MGI:1353631; Adat1.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADCB376 CRC64;
 Query Match 37.5%; Score 15; DB 11; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DQVA 6
 DB 5 DEIA 8
 RESULT 3
 Q8KMS9 PRELIMINARY; PRT; 7 AA.
 ID Q8KMS9
 AC Q8KMS9
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Putative transposase (Fragment).
 GN TNIA.
 OS Enterobacter sp. CH2-4.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=143777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CH2-4;
 RX MEDLINE=21604134; PubMed=11763242;
 RA Mindlin S.Z., Kholodil G.Y., Gorlenko Z.M., Minakhina S.V.,
 RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
 RA Yurieva O.V., Nikiforov V.G.;
 RT "Mercury resistance transposons of Gram-negative environmental
 RL bacteria and their classification.";
 RL Res. Microbiol. 152:811-822 (2001).
 DR EMBL; AJ302778; CAC83058.1; -.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;
 Query Match 35.0%; Score 14; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DQV 5
 DB 2 DQI 4
 RESULT 4
 Q99NX9 PRELIMINARY; PRT; 8 AA.
 ID Q99NX9
 AC Q99NX9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Amyloid beta protein (Fragment).
 GN APP.
 OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
 OX Hydrochoeris.
 OX NCBI_TaxID=10149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik B., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618 (2001).
 DR EMBL; AY011342; AAG47377.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 1071 MW; 1356D686DB19C9C3 CRC64;
 Query Match 35.0%; Score 14; DB 11; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLDQV 5
 DB 2 FFEQM 6
 RESULT 5
 Q9GD36 PRELIMINARY; PRT; 9 AA.
 ID Q9GD36
 AC Q9GD36
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein S16 (Fragment).
 GN RPS16.
 OS Juncus effusus (Soft rush).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.
 OX NCBI_TaxID=13579;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Asmussen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404962; CAC17904.1; -.
 DR GO; GO:0009507; Chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1135 MW; 8DCC9D2C046CB41 CRC64;
 Query Match 35.0%; Score 14; DB 8; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVAF 7
 DB 4 QIVF 7
 RESULT 6
 Q8JJ20 PRELIMINARY; PRT; 7 AA.
 ID Q8JJ20
 AC Q8JJ20
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Extracellular fatty acid binding protein (Fragment).
 GN EXFABP.
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wang Q., Li N., Li H.;
 RT "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF487519; AAL96665.1; --
 FT NON TER 1
 SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;

Query Match 32.5%; Score 13; DB 13; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LDQV 5
 DB 4 VDEV 7

RESULT 7

Q9RQ49
 ID Q9RQ49 PRELIMINARY; PRT; 8 AA.
 AC Q9RQ49
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN NIFS.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OC NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 compositions."
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AFI30814; AAF13805.1; --
 FT NON TER 8
 SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLD 3
 DB 6 YLD 8

RESULT 8

Q53790
 ID Q53790 PRELIMINARY; PRT; 8 AA.
 AC Q53790;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Lactose catabolic protein (LacZ) (Fragment).
 OS Streptococcus bovis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gilbert H.J., Hall J.;
 RT "Molecular cloning of Streptococcus bovis lactose catabolic genes."
 RL J. Gen. Microbiol. 133:2285-2293(1987).

DR EMBL; M35285; AAA36912.1; --
 DR PIR; A47618; A47618.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 863 MW; F95DC2D1AAB1A056 CRC64;

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DQVA 6
 DB 4 DTVA 7

RESULT 9

Q9RQ57
 ID Q9RQ57 PRELIMINARY; PRT; 8 AA.
 AC Q9RQ57;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN NIFS.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OC NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 compositions."
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AFI30812; AAF13797.1; --
 FT NON TER 8
 SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLD 3
 DB 6 YLD 8

RESULT 10

P82568
 ID P82568 PRELIMINARY; PRT; 9 AA.
 AC P82568;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN=URS4;
 RA Hogan D.A., Du P., Stevenson T.I., Whittom M., Kilby G.W., Rogers J.,
 RA VanBogelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 proteins."
 RL Submitted (MAY-2000) to Swiss-Prot.
 CC -1- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 32.5%; Score 13; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 1e+06; Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LDQV 5
:|:
Db 3 VDEV 6

RESULT 11

Q8H9Z1 PRELIMINARY; PRT; 9 AA.
AC Q8H9Z1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Capsid protein.
GN G20.
OS Cyanophage S-KM1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OC NCBI_TaxID=187678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S-KM1;
RA Okunishi S., Maeda H.;
RT "Cyanophage in Kagoshima Bay."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB080247; BAC54112.1;
SQ SEQUENCE 9 AA; 1167 MW; DB9205AB59DB42D6 CRC64;

Query Match 32.5%; Score 13; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVAF 7
:|:
Db 2 QVVF 5

RESULT 12

Q84333 PRELIMINARY; PRT; 9 AA.
AC Q84333;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Defective variant in 1443) with monkey alu-type insert (Fragment).
OS Simian virus 40 (SV40).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OC NCBI_TaxID=10633;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054804; PubMed=6254029;
RA Dhruva B.R., Shenk T., Subramanian K.N.;
RT "Integration in vivo into Simian virus 40 DNA of a sequence that resembles a certain family of genomic interspersed repeated sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).
DR EMBL: K01001; AAA47875.1; --
FT NON_TER
SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match 32.5%; Score 13; DB 12; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LDQV 5
:|:
Db 1 MDKV 4

RESULT 13

P72279
Query Match 30.0%; Score 12; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;

ID P72279 PRELIMINARY; PRT; 8 AA.
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Biphényl dioxygenase (fragment).
GN BPHB.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OC NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-positive bacterium Rhodococcus globerulus P6 to multicomponent dioxygenases of gram-negative bacteria."
RL Gene 156:11-18(1995).
DR EMBL: X80041; CAA56350.1; --
DR GO: GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KW Dioxygenase.
FT NON_TER
SQ SEQUENCE 8 AA; 989 MW; EBD2C81AB6D73406 CRC64;

Query Match 30.0%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDV 5
:|:
Db 5 DEV 7

RESULT 14

Q8GWM5 PRELIMINARY; PRT; 8 AA.
AC Q8GWM5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transposase (fragment).
GN TNP17.
OS Acinetobacter sp. BW3.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OC NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLM207;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLM2-like aberrant transposons and possible mechanisms of their dissemination."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLM207;
RA Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in the Acinetobacter genus."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250234; CAC80784.1; --
DR EMBL: AJ486856; CAD31078.1; --
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 30.0%; Score 12; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDQV 5
| |
Db 3 LTQV 6

RESULT 15

Q99MH2
ID Q99MH2 PRELIMINARY; PRT; 8 AA.
AC Q99MH2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Cyclooxygenase 2 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Claycombe K.J., Paulson E., Wu D., Meydani S.N.;
RT "Mouse cyclooxygenase 2 (COX-2) gene expression regulation."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF344876; AAK27680.1; -.
FT NON_TER 1 8
FT NON_TER 1 8
SQ SEQUENCE 8 AA; 911 MW; AC087DD046C411BA CRC64;

Query Match 30.0%; Score 12; DB 11; Length 8;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVA 6
| : |
Db 4 QIA 6

Search completed: February 24, 2004, 22:56:52
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2004, 22:26:09 ; Search time 52 Seconds
(without alignments)
48.902 Million cell updates/sec

Title: US-09-920-480B-1

Perfect score: 40

Sequence: 1 FLDQVAFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	97.5	9	5 AAU09698	Aau09698 Anti-mela
2	38	95.0	9	3 AAY84764	Aay84764 Antigenic
3	38	95.0	9	3 AAY84763	Aay84763 Antigenic
4	38	95.0	9	5 AAU09697	Aau09697 Anti-mela
5	34	85.0	9	2 AAR84835	Aar84835 Modified
6	34	85.0	9	3 AAY84766	Aay84766 Antigenic
7	34	85.0	9	4 AAU28984	Aau28984 Modified
8	34	85.0	9	5 AAU09696	Aau09696 Anti-mela
9	34	85.0	9	7 ADB97751	Adb97751 Human gpl
10	31	77.5	9	2 AAR84836	Aar84836 Modified
11	31	77.5	9	4 AAU28985	Aau28985 Modified
12	31	77.5	9	7 ADB97752	Adb97752 Human gpl
13	29	72.5	9	2 AAR84834	Aar84834 Modified
14	29	72.5	9	2 AAR84819	Aar84819 Modified
15	29	72.5	9	3 AAY84769	Aay84769 Antigenic
16	29	72.5	9	4 AAU28983	Aau28983 Modified
17	29	72.5	9	4 AAU28968	Aau28968 Modified
18	29	72.5	9	7 ADB97735	Adb97735 Human gpl
19	29	72.5	9	7 ADB97750	Adb97750 Human gpl
20	28	70.0	9	2 AAR84815	Aar84815 Modified
21	28	70.0	9	2 AAY55577	Aay55577 HLA bindi
22	28	70.0	9	2 AAY55434	Aay55434 HLA bindi
23	28	70.0	9	2 AAY55525	Aay55525 HLA bindi
24	28	70.0	9	4 AAU28965	Aau28965 Modified
25	28	70.0	9	4 AAB47533	Aab47533 Anti-mela

26	28	70.0	9	7 ADB97732	Adb97732 Human gpl
27	27	67.5	9	3 AAY84768	Aay84768 Antigenic
28	27	67.5	9	3 AAY84767	Aay84767 Antigenic
29	27	67.5	9	5 AAU09700	Aau09700 Anti-mela
30	26	65.0	9	2 AAR84821	Aar84821 Modified
31	26	65.0	9	2 AAR84817	Aar84817 Modified
32	26	65.0	9	2 AAR84818	Aar84818 Modified
33	26	65.0	9	4 AAU28970	Aau28970 Modified
34	26	65.0	9	4 AAU28967	Aau28967 Modified
35	26	65.0	9	4 AAU28966	Aau28966 Modified
36	26	65.0	9	4 AAB47536	Aab47536 Anti-mela
37	26	65.0	9	4 AAB47537	Aab47537 Anti-mela
38	26	65.0	9	4 AAU72002	Aau72002 gp100 mel
39	26	65.0	9	4 AAU10221	Aau10221 Cancer ce
40	26	65.0	9	4 AAE05120	Aae05120 Modified
41	26	65.0	9	5 AA017085	Aao17085 Gp 100 an
42	26	65.0	9	5 AAE17297	Aae17297 gp100-mod
43	26	65.0	9	6 AAE36055	Aae36055 tumour as
44	26	65.0	9	6 AAG79857	Aag79857 HLA-A2-re
45	26	65.0	9	6 AAE35575	Aae35575 Melanoma

ALIGNMENTS

RESULT 1

AAU09698

ID AAU09698 standard; peptide; 9 AA.

XX AC AAU09698;

XX DT 26-MAR-2002 (first entry)

XX DE Anti-melanoma compound #3.

XX KW Human; anti-melanoma compound; melanoma antigen gp100; APC; MHC; mutein;

XX KW Immune effector cell; antigen presenting cell; anti-cancer; mutant;

XX KW Major histocompatibility complex; gp100 tumour antigen; cytostatic.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200192294-A2.

XX PD 06-DEC-2001.

XX PF 21-MAY-2001; 2001WO-US016417.

XX PR 31-MAY-2000; 2000US-0208955P.

XX PA 09-FEB-2001; 2001US-0267877P.

XX PI (GENZ) GENZYME CORP.

XX PI Nicolette CA;

XX DR WPI; 2002-106301/14.

XX PT Novel anti-melanoma compound or peptide useful for inducing immune

XX PT response in a subject, for treating melanoma, as components of anti-

XX PT cancer vaccines and to expand immune effector cells specific for cancers.

XX PS Claim 3; Page 56; 69pp; English.

XX CC The present invention relates to anti-melanoma compounds comprising a

XX CC peptide sequence based on human melanoma antigen gp100. Also described

XX CC are antibodies that recognise and bind to these compounds,

XX CC polynucleotides that encode these compounds, and immune effector cells

XX CC that have been raised in vitro or in vivo in the presence of an antigen

XX CC presenting cell (APC) that presents the compound. Such an APC may be the

XX CC major histocompatibility complex (MHC) molecule. The anti-melanoma

XX CC compounds are useful for inducing an immune response in a subject, by

XX CC delivering the compound to the subject in the context of an MHC molecule

XX CC which presents the compound on the surface of an APC. The anti-melanoma

CC compound is delivered as a polynucleotide that encodes it. The compounds
 CC are useful to generate antibodies that specifically recognise and bind to
 CC them, for the treatment of melanoma, as components of anti-cancer
 CC vaccines, and to expand immune effector cells that are specific for
 CC cancers characterised by expression of gp100 tumour antigen, melanoma.
 CC The compounds are also useful in diagnostic methods for such diseases.
 CC AAU09696-AAU09705 represent the anti-melanoma compounds of the invention
 CC encoded by degenerate DNA sequences as shown in AAS14397-AAS14406
 CC respectively

XX SQ Sequence 9 AA;

Query Match 97.5%; Score 39; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLDQVAFV 9
 |||||
 Db 1 FLDQVAFSV 9

RESULT 2

AAAY84764
 ID AAAY84764 standard; peptide; 9 AA.

XX AC AAAY84764;

DT 08-AUG-2000 (first entry)

XX Antigenic peptide epitope of gp100 polypeptide.

XX Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 XX tumour antigen; vaccine; tumour cell; immune response; gp100.

XX Synthetic.

XX WO200020457-A1.

XX 13-APR-2000.

XX 04-OCT-1999; 99WO-US023167.

XX 05-OCT-1998; 98US-0103229P.

XX 05-JAN-1999; 99US-0114811P.

XX 11-FEB-1999; 99US-0120001P.

XX 11-FEB-1999; 99US-0120002P.

XX (GENZ) GENZYME CORP.

XX Nicolette CA;

XX WPI; 2000-303749/26.

XX Claim 11; Page 92; 116pp; English.

XX AAAY84763-69 represent synthetic antigenic peptide epitopes of gp100. The
 XX specification also describes synthetic epitopes of insulin-like growth
 XX factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class
 XX I or class II molecule with a higher affinity than the natural sequence.
 XX The synthetic antigenic peptide epitopes may correspond to tumour
 XX antigens, and are therefore useful as vaccines against tumour cells
 XX expressing cell surface tumour antigen. They are also useful in a variety
 XX of methods of modulating an immune response to the synthetic antigenic
 XX peptide epitopes and thus to the corresponding native antigenic
 XX determinant. The synthetic antigenic peptide epitopes find application in
 XX a wide variety of immunomodulatory protocols, including methods to induce
 XX or increase an immune response, as well as in methods to suppress or
 XX reduce an undesirable immune response to a corresponding natural epitope

SQ Sequence 9 AA;

Query Match 95.0%; Score 38; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLDQVAFV 9
 |||||
 Db 1 FLDQVAFV 9

RESULT 3

AAAY84763
 ID AAAY84763 standard; peptide; 9 AA.

XX AC AAAY84763;

DT 08-AUG-2000 (first entry)

XX Antigenic peptide epitope of gp100 polypeptide.

XX Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 XX tumour antigen; vaccine; tumour cell; immune response; gp100.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 8 /note= "any amino acid"

XX WO200020457-A1.

XX 13-APR-2000.

XX 04-OCT-1999; 99WO-US023167.

XX 05-OCT-1998; 98US-0103229P.

XX 05-JAN-1999; 99US-0114811P.

XX 11-FEB-1999; 99US-0120001P.

XX 11-FEB-1999; 99US-0120002P.

XX (GENZ) GENZYME CORP.

XX Nicolette CA;

XX WPI; 2000-303749/26.

XX New synthetic antigenic peptide epitopes related to insulin-like growth
 XX factor receptor, useful as vaccines against tumor cells expressing cell
 XX surface tumor antigen.

XX Claim 9; Page 91; 116pp; English.

XX AAAY84763-69 represent synthetic antigenic peptide epitopes of gp100. The
 XX specification also describes synthetic epitopes of insulin-like growth
 XX factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class
 XX I or class II molecule with a higher affinity than the natural sequence.
 XX The synthetic antigenic peptide epitopes may correspond to tumour
 XX antigens, and are therefore useful as vaccines against tumour cells
 XX expressing cell surface tumour antigen. They are also useful in a variety
 XX of methods of modulating an immune response to the synthetic antigenic
 XX peptide epitopes and thus to the corresponding native antigenic
 XX determinant. The synthetic antigenic peptide epitopes find application in
 XX a wide variety of immunomodulatory protocols, including methods to induce
 XX or increase an immune response, as well as in methods to suppress or
 XX reduce an undesirable immune response to a corresponding natural epitope

XX SQ Sequence 9 AA;

Query Match 95.0%; Score 38; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLDQVAFV 9
 |||||
 Db 1 FLDQVAFV 9

RESULT 4
 AAU09697
 ID AAU09697 standard; peptide; 9 AA.
 XX
 AC AAU09697;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Anti-melanoma compound #2.
 XX
 KW Human; anti-melanoma compound; melanoma antigen gp100; APC; MHC; mutein;
 KW immune effector cell; antigen presenting cell; anti-cancer; mutant;
 KW major histocompatibility complex; gp100 tumour antigen; cytostatic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200192294-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 21-MAY-2001; 2001WO-US016417.
 XX
 PR 31-MAY-2000; 2000US-0208955P.
 PR 09-FEB-2001; 2001US-0267877P.
 XX
 PA (GENZ) GENZYME CORP.
 XX
 PI Nicolette CA;
 XX
 DR WPI; 2002-106301/14.
 XX

Novel anti-melanoma compound or peptide useful for inducing immune response in a subject, for treating melanoma, as components of anti-cancer vaccines and to expand immune effector cells specific for cancers.
 Claim 2; Page 56; 69pp; English.
 The present invention relates to anti-melanoma compounds comprising a peptide sequence based on human melanoma antigen gp100. Also described are antibodies that recognise and bind to these compounds, polynucleotides that encode these compounds, and immune effector cells that have been raised in vitro or in vivo in the presence of an antigen presenting cell (APC) that presents the compound. Such an APC may be the major histocompatibility complex (MHC) molecule. The anti-melanoma compounds are useful for inducing an immune response in a subject, by delivering the compound to the subject in the context of an MHC molecule which presents the compound on the surface of an APC. The anti-melanoma compound is delivered as a polynucleotide that encodes it. The compounds are useful to generate antibodies that specifically recognise and bind to them, for the treatment of melanoma, as components of anti-cancer vaccines, and to expand immune effector cells that are specific for cancers characterised by expression of gp100 tumour antigen, melanoma. The compounds are also useful in diagnostic methods for such diseases. AAU09696-AAU09705 represent the anti-melanoma compounds of the invention encoded by degenerate DNA sequences as shown in AAS14397-AAS14406 respectively
 Sequence 9 AA;

Query Match 95.0%; Score 38; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLDQVAFV 9
 |||||
 Db 1 FLDQVAFV 9

RESULT 5
 AAR84835
 ID AAR84835 standard; peptide; 9 AA.
 XX
 AC AAR84835;
 XX
 DT 25-APR-1996 (first entry)
 XX
 DE Modified melanocyte-melanoma specific antigenic peptide G9-209-1F2L.
 XX
 KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;
 KW metastatic melanoma; tumour-associated antigen; immunogenic peptide;
 KW diagnosis; prognosis; prophylaxis; therapy; vaccine.
 XX
 OS Synthetic.
 XX
 PN WO9529193-A2.
 XX
 PD 02-NOV-1995.
 XX
 PF 21-APR-1995; 95WO-US005063.
 XX
 PR 22-APR-1994; 94US-00231565.
 PR 05-APR-1995; 95US-00417174.
 XX
 PA (USSH) US SEC DEPT HEALTH.
 XX
 PI Kawakami Y, Rosenberg SA;
 XX
 DR WPI; 1995-382963/49.
 XX
 PT DNA encoding melanoma antigens recognised by T-lymphocytes - also
 PT vectors, host cells and antibodies, used to detect, treat and immunise
 PT animal against melanoma.
 XX
 PS Example 5; Page 107; 184pp; English.
 XX

AAR84836-836 are G9-209 peptides modified to improve immunogenicity. G9-209 is an immunogenic peptide based on the melanoma derived antigen, gp100 (see AAR84210). The peptides are used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma)

SQ Sequence 9 AA;

Query Match 85.0%; Score 34; DB 2; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDQVAFV 9
 |||||
 Db 1 FLDQVPFSV 9

RESULT 6
 AAY84766
 ID AAY84766 standard; peptide; 9 AA.
 XX
 AC AAY84766;
 XX
 DT 08-AUG-2000 (first entry)
 XX

Antigenic peptide epitope of gp100 polypeptide.

Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 tumour antigen; vaccine; tumour cell; immune response; gp100.

Synthetic.

WO200020457-A1.

XX PD 13-APR-2000.
 XX PF 04-OCT-1999; 99WO-US023167.
 XX PR 05-OCT-1998; 98US-0103229P.
 XX PR 05-JAN-1999; 99US-0114811P.
 XX PR 11-FEB-1999; 99US-0120001P.
 XX PR 11-FEB-1999; 99US-0120002P.
 XX FA (GENZ) GENZYME CORP.
 XX PI Nicolette CA;
 XX DR WPI; 2000-303749/26.
 XX PT New synthetic antigenic peptide epitopes related to insulin-like growth
 XX PT factor receptor, useful as vaccines against tumor cells expressing cell
 XX PT surface tumor antigen.
 XX PS Claim 14; Page 92; 116pp; English.
 XX CC AY84763-69 represent synthetic antigenic peptide epitopes of gp100. The
 XX CC specification also describes synthetic epitopes of insulin-like growth
 XX CC factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class
 XX CC I or class II molecule with a higher affinity than the natural sequence.
 XX CC The synthetic antigenic peptide epitopes may correspond to tumour
 XX CC antigens, and are therefore useful as vaccines against tumour cells
 XX CC expressing cell surface tumour antigen. They are also useful in a variety
 XX CC of methods of modulating an immune response to the synthetic antigenic
 XX CC peptide epitopes and thus to the corresponding native antigenic
 XX CC determinant. The synthetic antigenic peptide epitopes find application in
 XX CC a wide variety of immunomodulatory protocols, including methods to induce
 XX CC or increase an immune response, as well as in methods to suppress or
 XX CC reduce an undesirable immune response to a corresponding natural epitope
 XX SQ Sequence 9 AA;
 Query Match 85.0%; Score 34; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FLDQVAFKV 9
 Db 1 FLDQVPPSV 9
 RESULT 7
 AAU28984
 ID AAU28984 standard; peptide; 9 AA.
 AC AAU28984;
 XX 18-DEC-2001 (first entry)
 XX DE Modified gp100 G9-209 peptide #20.
 XX KW Human; MART-I; immunogenic; melanoma antigen recognised by T lymphocyte;
 XX KW diagnostic; therapeutic; vaccine; melanoma, in vivo tumour recognition;
 XX KW in vivo tumour rejection.
 XX OS Synthetic.
 XX US6270778-B1.
 XX PN 07-AUG-2001.
 XX PD 12-MAR-1999; 99US-00267439.
 XX PF 22-APR-1994; 94US-00231565.
 XX PR 05-APR-1995; 95US-00417174.
 XX PR 05-MAY-1998; 98US-00073138.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Kawakami Y, Rosenberg SA;
 XX WPI; 2001-595403/67.
 XX DR Immunogenic peptide useful in vaccines comprises specific amino acids of
 XX PT new melanoma antigen recognized by T lymphocytes.
 XX PT Example 5; Col 55; 73pp; English.
 XX PS The invention relates to a novel immunogenic peptide comprising 5-20
 XX CC contiguous amino acids of new melanoma antigen recognised by T
 XX CC lymphocytes (MART-1). The peptide sequence contains at least one amino
 XX CC acid modification of MART-1. The peptide is used in diagnostic and
 XX CC therapeutic methods as an immunogen or vaccine to prevent or treat
 XX CC melanoma, and for in vivo tumour recognition and rejection. AAU28888-
 XX CC AAU29008 represent MART-1 peptide amino acid sequences, and related
 XX CC sequences of the invention
 XX SQ Sequence 9 AA;
 Query Match 85.0%; Score 34; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FLDQVAFKV 9
 Db 1 FLDQVPPSV 9
 RESULT 8
 AAU09696
 ID AAU09696 standard; peptide; 9 AA.
 XX AAU09696;
 XX 26-MAR-2002 (first entry)
 XX DE Anti-melanoma compound #1.
 XX KW Human; anti-melanoma compound; melanoma antigen gp100; APC; MHC; murein;
 XX KW immune effector cell; antigen presenting cell; anti-cancer; mutant;
 XX KW major histocompatibility complex; gp100 tumour antigen; cytostatic.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200192294-A2.
 XX PD 06-DEC-2001.
 XX PF 21-MAY-2001; 2001WO-US016417.
 XX PR 31-MAY-2000; 2000US-0208955P.
 XX PR 09-FEB-2001; 2001US-0267877P.
 XX PA (GENZ) GENZYME CORP.
 XX PI Nicolette CA;
 XX DR WPI; 2002-106301/14.
 XX PT Novel anti-melanoma compound or peptide useful for inducing immune
 XX PT response in a subject, for treating melanoma, as components of anti-
 XX PT cancer vaccines and to expand immune effector cells specific for cancers.
 XX PS Claim 1; Page 56; 69pp; English.
 XX CC The present invention relates to anti-melanoma compounds comprising a
 XX CC peptide sequence based on human melanoma antigen gp100. Also described
 XX CC are antibodies that recognise and bind to these compounds,
 XX CC polynucleotides that encode these compounds, and immune effector cells

CC that have been raised in vitro or in vivo in the presence of an antigen
 CC presenting cell (APC) that presents the compound. Such an APC may be the
 CC major histocompatibility complex (MHC) molecule. The anti-melanoma
 CC compounds are useful for inducing an immune response in a subject, by
 CC delivering the compound to the subject in the context of an MHC molecule
 CC which presents the compound on the surface of an APC. The anti-melanoma
 CC compound is delivered as a polynucleotide that encodes it. The compounds
 CC are useful to generate antibodies that specifically recognise and bind to
 CC them, for the treatment of melanoma, as components of anti-cancer
 CC vaccines, and to expand immune effector cells that are specific for
 CC cancers characterised by expression of gp100 tumour antigen, melanoma.
 CC The compounds are also useful in diagnostic methods for such diseases.
 CC AAU09696-AAU09705 represent the anti-melanoma compounds of the invention
 CC encoded by degenerate DNA sequences as shown in AAS14397-AAS14406
 CC respectively
 XX
 SQ Sequence 9 AA;

Query Match 85.0%; Score 34; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDQVAFVX 9
 |||||
 Db 1 FLDQVPFSV 9

RESULT 9
 ADB97751
 ID ADB97751 standard; peptide; 9 AA.

AC ADB97751;

DT 04-DEC-2003 (first entry)

XX Human gp100 antigenic peptide #12 analogue #20.

XX Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma;
 KW skin cancer; T lymphocyte; cytostatic; gene therapy; vaccine; antigen;
 KW major histocompatibility complex; MHC; human leukocyte antigen; HLA-A2;
 KW tumour infiltrating lymphocyte; mutant; mutein.

XX Synthetic.

OS Homo sapiens.

PN US2003144482-A1.

XX 31-JUL-2003.

XX 03-JUL-2001; 2001US-00898860.

XX 22-APR-1994; 94US-00231565.

XX 12-MAR-1999; 99US-00267439.

XX (KAWA/) KAWAKAMI Y.

PA (ROSE/) ROSENBERG S A.

XX Kawakami Y, Rosenberg SA;

XX WPI; 2003-755536/71.

PT New immunogenic peptides derived from melanoma antigens recognized by T-
 PT lymphocytes or from gp100, useful for preventing or treating melanoma.

XX Example 5; Page 31; 77pp; English.

XX The invention relates to an immunogenic peptide having contiguous amino
 CC acids derived from the sequence of melanoma antigens recognised by T-
 CC lymphocytes (MART-1) or gp100. The MART-1 sequence appears as ADB97651,
 CC and the gp100 (differing by 1 amino acid from the previously published
 CC gp100 (ADB97770) appears as ADB97676. Also included are a pharmaceutical
 CC composition (comprising the above peptide and an excipient, diluent or
 CC carrier), a vaccine for immunising a mammal (comprising the above peptide

CC in a carrier), preventing or treating melanoma (comprising administering
 CC the above composition to a mammal in an amount to stimulate the
 CC production of protective antibodies or immune cells), a purified and
 CC isolated nucleic acid sequence encoding the above peptide, a recombinant
 CC expression vector comprising at least one nucleic acid sequence cited
 CC above, a host organism transformed or transfected with the vector
 CC (expressing the peptide) and antibodies reactive with the above
 CC immunogenic peptide. The peptide sequence contains at least one amino
 CC acid modification (amino acid substitution) of the MART-1 or gp100
 CC sequence to enhance binding of the peptide to a Major Histocompatibility
 CC Complex (MHC) molecule. The peptide is recognised by Human Leukocyte
 CC Antigen (HLA)-A2 restricted tumour infiltrating lymphocytes. The
 CC composition and methods are useful in preventing or treating melanoma and
 CC skin cancer. The present sequence represents a modified melanoma
 CC antigenic peptide of the invention.

XX Sequence 9 AA;

Query Match 85.0%; Score 34; DB 7; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDQVAFVX 9
 |||||
 Db 1 FLDQVPFSV 9

RESULT 10

AAR84836

ID AAR84836 standard; peptide; 9 AA.

AC AAR84836;

DT 25-APR-1996 (first entry)

XX Modified melanocyte-melanoma specific antigenic peptide G9-209-1Y2L.

XX MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;

XX metastatic melanoma; tumour-associated antigen; immunogenic peptide;

XX diagnosis; prognosis; prophylaxis; therapy; vaccine.

XX Synthetic.

XX WO9529193-A2.

XX 02-NOV-1995.

XX 21-APR-1995; 95WO-US005063.

XX 22-APR-1994; 94US-00231565.

XX 05-APR-1995; 95US-00417174.

XX (USSH) US SEC DEPT HEALTH.

XX Kawakami Y, Rosenberg SA;

XX WPI; 1995-382963/49.

XX DNA encoding melanoma antigens recognised by T-lymphocytes - also
 XX vectors, host cells and antibodies, used to detect, treat and immunise
 XX animal against melanoma.

XX Example 5; Page 107; 184pp; English.

XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-
 CC 209 is an immunogenic peptide based on the melanoma derived antigen,
 CC gp100 (see AAR84210). The peptides are used in medicaments for the
 CC treatment or prevention (by immunization) of melanoma. Antibodies against
 CC MART-1 and its immunogenic peptides may be used in the detection and
 CC isolation of MART-1 from a sample, the detection of which is indicative
 CC of a disease state (melanoma or metastatic melanoma)

XX Sequence 9 AA;

Query Match 77.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDOVAFKV 9
 :|||||
 Db 1 YLDQVPFSV 9

RESULT 11
 AAU28985
 ID AAU28985 standard; peptide; 9 AA.
 AC AAU28985;
 XX
 DT 18-DEC-2001 (first entry)
 DE Modified gp100 G9-209 peptide #21.
 KW Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;
 KW diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;
 KW in vivo tumour rejection.
 XX Synthetic.
 OS
 XX USG270778-B1.
 FN
 XX 07-AUG-2001.
 PD
 XX 12-MAR-1999; 99US-00267439.
 PF
 XX 22-APR-1994; 94US-00231565.
 PR
 XX 05-APR-1995; 95US-00417174.
 PR
 XX 05-MAY-1998; 98US-00073138.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kawakami Y, Rosenberg SA;
 XX WPI; 2001-595403/67.
 DR
 XX Immunogenic peptide useful in vaccines comprises specific amino acids of
 PT new melanoma antigen recognised by T lymphocytes.
 XX
 PS Example 5; Col 55; 73pp; English.
 XX
 CC The invention relates to a novel immunogenic peptide comprising 5-20
 CC contiguous amino acids of new melanoma antigen recognised by T
 CC lymphocytes (MART-1). The peptide sequence contains at least one amino
 CC acid modification of MART-1. The peptide is used in diagnostic and
 CC therapeutic methods as an immunogen or vaccine to prevent or treat
 CC melanoma, and for in vivo tumour recognition and rejection. AAU28988-
 CC AAU29008 represent MART-1 peptide amino acid sequences, and related
 CC sequences of the invention
 XX
 SQ Sequence 9 AA;

Query Match 77.5%; Score 31; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDOVAFKV 9
 :|||||
 Db 1 YLDQVPFSV 9

RESULT 12
 ADB97752
 ID ADB97752 standard; peptide; 9 AA.
 XX
 AC ADB97752;
 XX

DT 04-DEC-2003 (first entry)
 XX
 DE Human gp100 antigenic peptide #12 analogue #21.
 XX
 KW Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma;
 KW skin cancer; T lymphocyte; cytostatic; gene therapy; vaccine; antigen;
 KW major histocompatibility complex; MHC; human leukocyte antigen; HLA-A2;
 KW tumour infiltrating lymphocyte; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN US2003144482-A1.
 XX
 XX 31-JUL-2003.
 PD
 XX 03-JUL-2001; 2001US-00898860.
 PF
 XX 22-APR-1994; 94US-00231565.
 PR
 XX 12-MAR-1999; 99US-00267439.
 XX
 PA (KAWA/) KAWAKAMI Y.
 PA (ROSE/) ROSENBERG S A.
 XX
 PI Kawakami Y, Rosenberg SA;
 XX WPI; 2003-755536/71.
 DR
 XX New immunogenic peptides derived from melanoma antigens recognized by T-
 PT lymphocytes or from gp100, useful for preventing or treating melanoma.
 XX
 PS Example 5; Page 31; 77pp; English.
 XX
 CC The invention relates to an immunogenic peptide having contiguous amino
 CC acids derived from the sequence of melanoma antigens recognised by T-
 CC lymphocytes (MART-1) or gp100. The MART-1 sequence appears as ADB97651,
 CC and the gp100 (differing by 1 amino acid from the previously published
 CC gp100 (ADB97770) appears as ADB97676. Also included are a pharmaceutical
 CC composition (comprising the above peptide and an excipient, diluent or
 CC carrier), a vaccine for immunising a mammal (comprising the above peptide
 CC in a carrier), preventing or treating melanoma (comprising administering
 CC the above composition to a mammal in an amount to stimulate the
 CC production of protective antibodies or immune cells), a purified and
 CC isolated nucleic acid sequence encoding the above peptide, a recombinant
 CC expression vector comprising at least one nucleic acid sequence cited
 CC above, a host organism transformed or transfected with the vector
 CC (expressing the peptide) and antibodies reactive with the above
 CC immunogenic peptide. The peptide sequence contains at least one amino
 CC acid modification (amino acid substitution) of the MART-1 or gp100
 CC sequence to enhance binding of the peptide to a Major Histocompatibility
 CC Complex (MHC) molecule. The peptide is recognised by Human Leukocyte
 CC Antigen (HLA)-A2 restricted tumour infiltrating lymphocytes. The
 CC composition and methods are useful in preventing or treating melanoma and
 CC skin cancer. The present sequence represents a modified melanoma
 CC antigenic peptide of the invention.

Sequence 9 AA;

Query Match 77.5%; Score 31; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLDOVAFKV 9
 :|||||
 Db 1 YLDQVPFSV 9

RESULT 13
 AAR84834
 ID AAR84834 standard; peptide; 9 AA.
 XX
 AC AAR84834;
 XX

```

DT XX 25-APR-1996 : (first entry)
DE XX Modified melanocyte-melanoma specific antigenic peptide G9-209-1W2L.
XX
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;
KW metastatic melanoma; tumour-associated antigen; immunogenic peptide;
KW diagnosis; prognosis; prophylaxis; therapy; vaccine.
XX
OS Synthetic.
XX
XX WO9529193-A2.
XX
XX 02-NOV-1995.
XX
XX 21-APR-1995; 95WO-US005063.
XX
XX 22-APR-1994; 94US-00231565.
XX
XX 05-APR-1995; 95US-00417174.
XX
XX (USSH ) US SEC DEPT HEALTH.
XX
XX Kawakami Y, Rosenberg SA;
XX
XX WPI; 1995-382963/49.
XX
XX DNA encoding melanoma antigens recognised by T-lymphocytes - also
XX vectors, host cells and antibodies, used to detect, treat and immunise
XX animal against melanoma.
XX
XX Example 5; Page 107; 184pp; English.
XX
XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-
XX 209 is an immunogenic peptide based on the melanoma derived antigen,
XX gp100 (see AAR84210). The peptides are used in medicaments for the
XX treatment or prevention (by immunization) of melanoma. Antibodies against
XX MART-1 and its immunogenic peptides may be used in the detection and
XX isolation of MART-1 from a sample, the detection of which is indicative
XX of a disease state (melanoma or metastatic melanoma)
XX
XX Sequence 9 AA;
XX
XX Query Match 72.5%; Score 29; DB 2; Length 9;
XX Best Local Similarity 66.7%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 FLDQVAFXY 9
XX :|||||
XX 1 FLDQVFPFV 9
XX
XX Db
XX
XX RESULT 15
XX AAR84769
XX ID AAY84769 standard; peptide; 9 AA.
XX
XX AC AAY84769;
XX
XX DT 08-AUG-2000 (first entry)
XX
XX DE Antigenic peptide epitope of gp100 polypeptide.
XX
XX KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
XX tumour antigen; vaccine; tumour cell; immune response; gp100.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 5 /note= "any amino acid"
XX FT Misc-difference 6 /note= "any amino acid"
XX FT Misc-difference 8 /note= "any amino acid"
XX
XX PN WO200020457-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 04-OCT-1999; 99WO-US023167.
XX
XX PR 05-OCT-1998; 98US-0103229P.
XX PR 05-JAN-1999; 99US-0114811P.
XX PR 11-FEB-1999; 99US-0120001P.
XX PR 11-FEB-1999; 99US-0120002P.
XX
XX PA (GENZ ) GENZYME CORP.
XX
XX PI Nicolette CA;
XX
XX DR WPI; 2000-303749/26.
XX
XX

```

```

DT XX 25-APR-1996 : (first entry)
DE XX Modified melanocyte-melanoma specific antigenic peptide G9-209-1W2L.
XX
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;
KW metastatic melanoma; tumour-associated antigen; immunogenic peptide;
KW diagnosis; prognosis; prophylaxis; therapy; vaccine.
XX
OS Synthetic.
XX
XX WO9529193-A2.
XX
XX 02-NOV-1995.
XX
XX 21-APR-1995; 95WO-US005063.
XX
XX 22-APR-1994; 94US-00231565.
XX
XX 05-APR-1995; 95US-00417174.
XX
XX (USSH ) US SEC DEPT HEALTH.
XX
XX Kawakami Y, Rosenberg SA;
XX
XX WPI; 1995-382963/49.
XX
XX DNA encoding melanoma antigens recognised by T-lymphocytes - also
XX vectors, host cells and antibodies, used to detect, treat and immunise
XX animal against melanoma.
XX
XX Example 5; Page 107; 184pp; English.
XX
XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-
XX 209 is an immunogenic peptide based on the melanoma derived antigen,
XX gp100 (see AAR84210). The peptides are used in medicaments for the
XX treatment or prevention (by immunization) of melanoma. Antibodies against
XX MART-1 and its immunogenic peptides may be used in the detection and
XX isolation of MART-1 from a sample, the detection of which is indicative
XX of a disease state (melanoma or metastatic melanoma)
XX
XX Sequence 9 AA;
XX
XX Query Match 72.5%; Score 29; DB 2; Length 9;
XX Best Local Similarity 66.7%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 FLDQVAFXY 9
XX :|||||
XX 1 WLDQVFPFV 9
XX
XX Db
XX
XX RESULT 14
XX AAR84819
XX ID AAR84819 standard; peptide; 9 AA.
XX
XX AC AAR84819;
XX
XX DT 25-APR-1996 (first entry)
XX
XX DE Modified melanocyte-melanoma specific antigenic peptide G9-209-1F.
XX
XX KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;
KW metastatic melanoma; tumour-associated antigen; immunogenic peptide;
KW diagnosis; prognosis; prophylaxis; therapy; vaccine.
XX
XX OS Synthetic.
XX
XX PN WO9529193-A2.
XX
XX PD 02-NOV-1995.
XX
XX PF 21-APR-1995; 95WO-US005063.
XX
XX PR 22-APR-1994; 94US-00231565.
XX

```

PT New synthetic antigenic peptide epitopes related to insulin-like growth
PT factor receptor, useful as vaccines against tumor cells expressing cell
PT surface tumor antigen.

XX
XX
PS Claim 17; Page 92; 116pp; English.

XX
CC AAY84763-69 represent synthetic antigenic peptide epitopes of gp100. The
CC specification also describes synthetic epitopes of insulin-like growth
CC factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class
CC I or class II molecule with a higher affinity than the natural sequence.
CC The synthetic antigenic peptide epitopes may correspond to tumour
CC antigens, and are therefore useful as vaccines against tumour cells
CC expressing cell surface tumour antigen. They are also useful in a variety
CC of methods of modulating an immune response to the synthetic antigenic
CC peptide epitopes and thus to the corresponding native antigenic
CC determinant. The synthetic antigenic peptide epitopes find application in
CC a wide variety of immunomodulatory protocols, including methods to induce
CC or increase an immune response, as well as in methods to suppress or
CC reduce an undesirable immune response to a corresponding natural epitope
XX
SQ Sequence 9 AA;

Query Match 72.5%; Score 29; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FLDQVAFXY 9
Db 1 FLDQXXFXV 9

Search completed: February 24, 2004, 22:55:35
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:33:10 ; Search time 21 seconds
(without alignments)
41.225 Million cell updates/sec

Title: US-09-920-480B-3

Perfect score: 47
Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	55.3	9	2	146023
2	20	42.6	9	2	S56004
3	18	38.3	7	2	S21230
4	18	38.3	7	2	PN0649
5	18	38.3	8	2	JS0318
6	18	38.3	8	2	TL3818
7	18	38.3	9	2	A24244
8	16	34.0	8	2	S10596
9	16	34.0	8	2	B24749
10	15	31.9	4	2	PT0661
11	15	31.9	5	2	PT0580
12	15	31.9	6	2	A31283
13	15	31.9	6	2	A61068
14	15	31.9	7	2	A61081
15	15	31.9	8	2	JS0315
16	15	31.9	8	2	JS0316
17	15	31.9	8	2	JS0317
18	15	31.9	8	2	A38887
19	15	31.9	9	2	D57444
20	15	31.9	9	2	PT0272
21	15	31.9	9	2	PT0299
22	15	31.9	9	2	PT0315
23	15	31.9	9	2	I58350
24	14	29.8	7	1	NYFG7
25	14	29.8	9	2	C24180
26	14	29.8	9	2	A43848
27	13	27.7	6	2	PD0028
28	13	27.7	7	2	PX0008
29	13	27.7	8	2	A28004

30 13 27.7 8 2 S08996 hypertrehalosemic
31 13 27.7 8 2 B49823 adipokinetic hormo
32 13 27.7 8 2 B44960 neuropeptide led-C
33 13 27.7 8 2 A39308 glycine reductase
34 13 27.7 8 2 S68325 blood cell protein
35 13 27.7 9 2 S78426 52.5K protein - sp
36 12 25.5 5 2 PT0281 Ig heavy chain CRD
37 12 25.5 6 2 S66195 alcohol dehydrogen
38 12 25.5 6 2 B31263 dihydrofolate redu
39 12 25.5 6 2 PT0532 T-cell receptor be
40 12 25.5 7 2 A58512 venom heptapeptide
41 12 25.5 7 2 S09652 hypothetical prote
42 12 25.5 7 2 PQ0727 H2 class I protein
43 12 25.5 7 4 A58725 virotoxin - destro
44 12 25.5 8 2 S08995 hypertrehalosemic
45 12 25.5 8 2 A49823 adipokinetic hormo

ALIGNMENTS

RESULT 1

I46023
growth hormone receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C;Accession: I46023
R;Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
Mol Cell Endocrinol. 72, 187-200, 1990
A;Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
A;Reference number: I46023; MUID:91146804; PMID:2289631
A;Accession: I46023
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-9 <HAU>
A;Cross-references: EMBL:U24113; NID:g775221; PIDN:AAA91014.1; PID:g775223
C;Genetics:
A;Gene: GHR

Query Match 55.3%; Score 26; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FLFSWYAXV 9
Db 1 FQFPWFVIV 9

RESULT 2

S56004
glucan 1,3-beta-glucosidase (EC 3.2.1.58) GNIII, extracellular - fungus (Acremonium pers
N;Alternate names: (1-3)-beta-D-glucan glucosylase GNIII
C;Species: Acremonium persicinum
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C;Accession: S56004
R;Pitson, S.M.; Seviour, R.J.; McDougall, B.M.; Woodward, J.R.; Stone, B.A.
Biochem. J. 308, 733-741, 1995
A;Title: Purification and characterization of three extracellular (1->3)-beta-D-glucan g
A;Reference number: S56002; MUID:97104268; PMID:8948426
A;Accession: S56004
A;Molecule type: protein
A;Residues: 1-9 <PIT>
C;Keywords: glycosidase; hydrolase

Query Match 42.6%; Score 20; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 WYAXV 9
Db 5 WFANI 9

RESULT 3

S21230
 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
 C;Accession: S21230
 R;Magnogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A;Title: Identification and characterization of two dermorphins from skin extracts of the
 A;Reference number: S21152; MUID:92339502; PMID:1633846
 A;Accession: S21230
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <MIG>
 C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 38.3%; Score 18; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WY 6
 ||
 ||
 Db 4 WY 5

RESULT 4

PN0649
 pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
 C;Species: Bacillus sp.
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
 C;Accession: PN0649
 R;Kim, C.H.; Choi, H.I.; Lee, D.S.
 Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
 A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalop
 A;Reference number: PN0649; MUID:94080025; PMID:7764261
 A;Accession: PN0649
 A;Molecule type: protein
 A;Residues: 1-7 <KIM>
 C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of su
 nent in high maltose syrups.
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 38.3%; Score 18; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SWY 6
 ||
 ||
 Db 5 SWF 7

RESULT 5

JS0318
 leucokinin VIII - Madeira cockroach
 C;Species: Leucophaea maderae (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0318
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 31-34, 1987
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
 A;Reference number: JS0317
 A;Accession: JS0318
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 38.3%; Score 18; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FSW 5

Db 5 YSW 7
 :||

RESULT 6

TI3818
 cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
 C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C;Accession: TI3818
 R;Delabre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
 Mol. Biol. Evol. 14, 807-813, 1997
 A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
 A;Reference number: Z17775; MUID:97398704; PMID:9254918
 A;Accession: TI3818
 A;Status: preliminary; translated from GB/EMBL/DBDB

A;Molecule type: DNA
 A;Residues: 1-8
 A;Cross-references: EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:g2340022
 C;Genetics:
 A;Genome: mitochondrion
 A;Note: COI
 C;Keywords: mitochondrion

Query Match 38.3%; Score 18; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLPSWY 6
 :||
 Db 2 YLSRWF 7

RESULT 7

A24244
 adipokinetic hormone - bollworm
 N;Alternate names: Hez-AKH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C;Accession: A24244
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic
 A;Reference number: A24244; MUID:86186794; PMID:3964263
 A;Accession: A24244
 A;Molecule type: protein
 A;Residues: 1-9 <JAF>

C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 38.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLPSW 5
 :||
 Db 4 FTSSW 8

RESULT 8

S10596
 adipokinetic hormone - pond skimmer
 C;Species: Libellula auripennis
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
 C;Accession: S10596
 R;Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hc
 A;Reference number: S10596; MUID:90359055; PMID:2390213
 A;Accession: S10596
 A;Molecule type: protein

A;Residues: 1-8 <BIO>
 C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLPSW 5
 DB 4 FTPSW 8

RESULT 9
 B24749
 neuropeptide B - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
 C;Accession: B24749
 R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
 A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two h
 A;Reference number: A94074; MUID:86067985; PMID:3865193
 A;Accession: B24749
 A;Molecule type: protein
 A;Residues: 1-8 <YAN>
 C;Superfamily: unassigned animal peptides
 C;Keywords: neuropeptide

Query Match 34.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLF 3
 DB 1 FLF 3

RESULT 10
 PT0661
 T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0661
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0661
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 4 postnatal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 31.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 DB 2 SW 3

RESULT 11
 PT0580
 T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0580

R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0580
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 31.9%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 DB 3 SW 4

RESULT 12
 A31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
 C;Species: Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C;Accession: A31263
 R;Peterson, D.S.; Walliker, D.; Wellem, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A;Reference number: A94217; MUID:89057886; PMID:2904149
 A;Accession: A31263
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PET>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 31.9%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 DB 2 SW 3

RESULT 13
 A61068
 locustakinin - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
 C;Accession: A61068
 R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
 Regul. Pept. 37, 49-57, 1992
 A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri
 A;Reference number: A61068; MUID:92262851; PMID:1585017
 A;Accession: A61068
 A;Molecule type: protein
 A;Residues: 1-6 <SCH>
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
 F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.9%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 DB 4 SW 5

RESULT 14
 A61081
 tryptophyllin, basic - Rohde's leaf frog

C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C:Accession: A61081
 R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 33, 391-395, 1989
 A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containing
 A:Reference number: A61081
 A:Accession: A61081
 A:Molecule type: protein
 A:Residues: 1-7 <MON>
 C:Comment: The biological activity of this peptide was not determined.
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; hydroxyproline; skin
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.9%; Score 15; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 ||
 Db 4 SW 5

RESULT 15
 JS0315
 leucokinin V - Madeira cockroach
 C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0315
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
 A:Reference number: JS0315
 A:Accession: JS0315
 A:Molecule type: protein
 A:Residues: 1-8 <HOL>
 C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide
 F:3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.9%; Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 ||
 Db 6 SW 7

Search completed: March 18, 2004, 13:36:55
 Job time : 22 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:29:30 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-920-480B-3

Perfect score: 47

Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	38.3	8	1 LCK8_LEUMA	P19990 leucophaea
2	16	34.0	7	1 PPH2_LYCES	P83379 lycopersico
3	16	34.0	8	1 AKH_LIBAU	P25418 libellula a
4	16	34.0	8	1 NPMB_BOVIN	P15507 bos taurus
5	16	34.0	9	1 NEUU_CAVPO	P34966 cavia porce
6	15	31.9	4	1 OCP3_OCTMI	P58649 octopus min
7	15	31.9	6	1 LOK1_LOEMI	P41491 locusta mig
8	15	31.9	8	1 LCK1_LEUMA	P21140 leucophaea
9	15	31.9	8	1 LCK2_LEUMA	P21141 leucophaea
10	15	31.9	8	1 LCK3_LEUMA	P21142 leucophaea
11	15	31.9	8	1 LCK4_LEUMA	P21143 leucophaea
12	15	31.9	8	1 LCK5_LEUMA	P19987 leucophaea
13	15	31.9	8	1 LCK6_LEUMA	P19988 leucophaea
14	15	31.9	8	1 LCK7_LEUMA	P19989 leucophaea
15	14	29.8	7	1 HV7_PIG	P01153 sus scrofa
16	14	29.8	7	1 TV51_LITRU	P82065 litoria rub
17	14	29.8	8	1 CAD1_ENTFA	P13268 enterococcu
18	14	29.8	8	1 COM2_CONPU	P58785 conus purpu
19	14	29.8	9	1 FIBB_MACFU	P19345 macaca fusc
20	14	29.8	9	1 RT33_BOVIN	P82926 bos taurus
21	13	27.7	8	1 AKHG_GRYBI	P14086 gryllus bim
22	13	27.7	8	1 HTE2_PERAM	P04549 periplaneta
23	12	25.5	5	1 PAP2_PARMA	P81864 pardachirus
24	12	25.5	6	1 EI01_LITRU	P82096 litoria rub
25	12	25.5	7	1 BRHP_CONIM	P58803 conus imper
26	12	25.5	7	1 TPFY_PACDA	P83455 pachymedusa
27	12	25.5	8	1 AKH_TABAT	P14595 tabanus atr
28	12	25.5	8	1 HTF1_PERAM	P04548 periplaneta
29	12	25.5	8	1 HTF_TENMO	P25419 tenebrio mo
30	12	25.5	8	1 RT34_BOVIN	P82929 bos taurus
31	12	25.5	9	1 LMIP_LOEMI	P31799 locusta mig
32	12	25.5	9	1 PTSP_BOMMO	P82003 bombyx mori
33	11	23.4	5	1 BPP7_BOVIN	P30425 bothrops in

34	11	23.4	5	1 UP01_MOUSE	P38639 mus musculus
35	11	23.4	7	1 ALL2_CARMA	P81805 carcinus ma
36	11	23.4	7	1 ALL3_CARMA	P81806 carcinus ma
37	11	23.4	7	1 ALL4_CARMA	P81807 carcinus ma
38	11	23.4	7	1 ALL5_CARMA	P81808 carcinus ma
39	11	23.4	7	1 WWA1_ACHFUF	P35919 achatina fu
40	11	23.4	7	1 WWA2_ACHFUF	P35920 achatina fu
41	11	23.4	7	1 WWA3_ACHFUF	P35921 achatina fu
42	11	23.4	8	1 ACI_THUAL	P18691 thunnus alb
43	11	23.4	8	1 AKH_MELML	P25423 melolontha
44	11	23.4	8	1 ALL2_CARMA	P81815 carcinus ma
45	11	23.4	8	1 ALL7_CARMA	P81809 carcinus ma

ALIGNMENTS

RESULT 1
LCK8_LEUMA
ID LCK8_LEUMA STANDARD; PRT; 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Leucokinin VIII (L-VIII)
OS Leucophaea maderae (Madeira cockroach)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
VIII: the final members of this new family of cephalomyotropic
peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach prothoracic gland (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR Neuropeptide; Amidation.
KW PIR; JS0318; JS0319.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
AMIDATION.

Query Match 38.3%; Score 18; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FSW 5
DB 5 YSW 7

RESULT 2
PPH2_LYCES
ID PPH2_LYCES STANDARD; PRT; 7 AA.
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LesAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE. CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;

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RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 34.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLF 3
DB 1 FLF 3

RESULT 3
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]_TaxID=6966;
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596;
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuroptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 978 MW; 8665A771A3C452D6 CRC64;

Query Match 34.0%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLFSW 5
DB 4 FTFSW 8

RESULT 4
NPMB_BOVIN
ID NPMB_BOVIN STANDARD; PRT; 8 AA.

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AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Morphine modulating neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: Modulates the action of morphine.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 34.0%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLF 3
DB 1 FLF 3

RESULT 5
NEUU_CAVPO
ID NEUU_CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (NmU-9).
GN NMU.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]_TaxID=10141;
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90341105; PubMed=2381877;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT from guinea pig small intestine.";
RL Peptides 11:613-617(1990).
CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
CC selective vasoconstriction.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NmU family.
DR InterPro; IPR008199; NMU.
DR Pfam; PF02070; NMU; 1.
DR PROSITE; PS00967; NMU; 1.
KW Amidation; Hormone.
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

Query Match 34.0%; Score 16; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLF 3
DB 1 FLF 3

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Db          3 FLP 5

RESULT 6
OCP3_OCTMI
ID _OCP3_OCTMI      STANDARD;      PRT;      4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6A8365B810000000 CRC64;

Query Match          31.9%; Score 15; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 SW 5
Db          2 SW 3

RESULT 7
LOK1_LOCMI
ID _LOK1_LOCMI      STANDARD;      PRT;      6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC DR PIR: A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 SW 5
Db          6 SW 7

RESULT 8
LCK1_LEUMA
ID _LCK1_LEUMA      STANDARD;      PRT;      8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 SW 5
Db          6 SW 7

RESULT 9
LCK2_LEUMA
ID _LCK2_LEUMA      STANDARD;      PRT;      8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

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Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
      ||
Db      6 SW 7

RESULT 10
LCK3 LEUMA
ID LCK3 LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B49C866DA CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
      ||
Db      6 SW 7

RESULT 11
LCK4 LEUMA
ID LCK4 LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B49C866DA CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
      ||
Db      6 SW 7

RESULT 12
LCK5 LEUMA
ID LCK5 LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW PIR; JS0315; JS0315.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
      ||
Db      6 SW 7

RESULT 13
LCK6 LEUMA
ID LCK6 LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match          31.9%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
      ||
Db      6 SW 7

```

DR PIR; JS0316; JS0316.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;
 Query Match 31.9%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 SW 5
 ||
 Db 6 SW 7

RESULT 14
 LCK7 LEUMA
 ID LCK7 LEUMA STANDARD; PRT; 8 AA.
 AC P19989;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 VIII: the final members of this new family of cephalomyotropic
 peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 activity of cockroach prothorax (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDC76A CRC64;
 Query Match 31.9%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 SW 5
 ||
 Db 6 SW 7

RESULT 15
 HY7_PIG
 ID HY7_PIG STANDARD; PRT; 7 AA.
 AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Hypothalamic heptapeptide.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=81213980; PubMed=6263778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 RA Saffran M., Kong A., Hamilton J.W., Conn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro
 ACTH-releasing activity from porcine hypothalamus.";
 RL Horm. Metab. Res. 13:228-232(1981).

DR PIR; A01417; NYPG7.
 SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
 Query Match 29.8%; Score 14; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FLFSWY 6
 ||:
 Db 1 FIYHSY 6

Search completed: March 18, 2004, 13:35:31
 Job time : 12 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:32:50 ; Search time 38 Seconds
(without alignments)
74.728 Million cell updates/sec

Title: US-09-920-480B-3

Perfect score: 47

Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	55.3	9	6 Q28121	Q28121 bos taurus
2	18	38.3	8	8 Q94VF6	Q94VF6 varanus job
3	18	38.3	9	4 Q9UK44	Q9UK44 homo sapien
4	18	38.3	9	4 Q9UC36	Q9UC36 homo sapien
5	15	31.9	8	5 P82685	P82685 periplaneta
6	15	31.9	8	5 P82686	P82686 periplaneta
7	15	31.9	8	5 P82687	P82687 periplaneta
8	15	31.9	8	5 P82688	P82688 periplaneta
9	15	31.9	8	5 P82689	P82689 periplaneta
10	15	31.9	8	8 Q8WGD7	Q8WGD7 lomus hirta
11	15	31.9	8	8 Q94V88	Q94V88 varanus tri
12	15	31.9	8	8 Q94VY2	Q94VY2 asterina pe
13	15	31.9	8	8 Q94VJ4	Q94VJ4 varanus ben
14	15	31.9	8	8 Q94V91	Q94V91 varanus tim
15	15	31.9	8	8 Q94VE4	Q94VE4 varanus mel
16	15	31.9	8	8 Q94VF9	Q94VF9 varanus ind

17	15	31.9	8	12 Q64971	Q64971 alfalfa mos
18	15	31.9	9	8 Q8WFS4	Q8WFS4 diadema mex
19	15	31.9	9	8 Q9T688	Q9T688 gecko gecko
20	15	31.9	9	8 Q94VH4	Q94VH4 varanus gia
21	15	31.9	9	8 Q94VD8	Q94VD8 varanus nil
22	15	31.9	9	8 Q94VI8	Q94VI8 varanus ere
23	15	31.9	9	8 Q94VJ1	Q94VJ1 varanus dor
24	15	31.9	9	8 Q8W8W5	Q8W8W5 diadema set
25	15	31.9	9	8 Q8WGR6	Q8WGR6 procambatus
26	15	31.9	9	8 Q8W8W6	Q8W8W6 diadema ant
27	15	31.9	9	8 Q94VE1	Q94VE1 varanus mer
28	15	31.9	9	11 Q80X07	Q80X07 mus sp. thr
29	15	31.9	9	12 Q90350	Q90350 hepatitis g
30	14	29.8	8	8 Q8W8G2	Q8W8G2 diadema sav
31	14	29.8	8	8 Q8W8G4	Q8W8G4 diadema mex
32	14	29.8	8	8 Q9TD02	Q9TD02 terranatos
33	14	29.8	8	8 Q94VA0	Q94VA0 varanus sem
34	14	29.8	8	8 Q94PX5	Q94PX5 felis silve
35	14	29.8	8	8 Q8W8G5	Q8W8G5 diadema ant
36	14	29.8	8	8 Q8W8G3	Q8W8G3 diadema pau
37	14	29.8	8	8 Q94PX7	Q94PX7 felis silve
38	14	29.8	8	8 Q94PX6	Q94PX6 felis libyc
39	14	29.8	9	2 Q47063	Q47063 escherichia
40	14	29.8	9	2 Q9R5W1	Q9R5W1 staphylococ
41	14	29.8	9	2 Q8GLJ1	Q8GLJ1 borrelia bu
42	14	29.8	9	2 Q8GL26	Q8GL26 borrelia bu
43	14	29.8	9	8 Q8W8X4	Q8W8X4 diadema mex
44	14	29.8	9	12 Q89491	Q89491 murine minu
45	13	27.7	8	2 Q85406	Q85406 coxiella bu

ALIGNMENTS

RESULT 1

Q28121	Q28121	PRELIMINARY;	PRT;	9 AA.
AC	Q28121;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Growth hormone receptor (Fragment).			
GN	GHR.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96043217; PubMed=7486254;			
RA	Moody D.E., Pomp D., Barendse W., Momack J.E.;			
RT	"Assignment of the growth hormone receptor gene to bovine chromosome 20 using linkage analysis and somatic cell mapping.";			
RL	Anim. Genet. 26:341-343(1995).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91146804; PubMed=2289631;			
RA	Hauser S.D., McGrath M.F., Collier R.J., Krivi G.G.;			
RT	"Cloning and in vivo expression of bovine growth hormone receptor mRNA";			
RL	Mol. Cell. Endocrinol. 72:187-200(1990).			
DR	EMBL; U24113; AAA91014.1; -.			
DR	PIR; I46023; I46023.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
KW	Receptor.			
FT	NON_TER	1	1	
FT	NON_TER	9	9	
SQ	SEQUENCE	9 AA;	1182 MW;	D11E42C9D36769D6 CRC64;

Query Match 55.3%; Score 26; DB 6; Length 9;
Best Local Similarity 44.4%; Pred. No. 1e+06; 4; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FLESHYXV 9
Db      1 FQFPWFVIV 9

RESULT 2
Q94VF6 PRELIMINARY; PRT; 8 AA.
AC Q94VF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus jobiensis (Peach throat monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169843;
RN [1]_TaxID=169843;
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407507; AAL10075.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 1144 MW; EFD729DB436411A6 CRC64;

Query Match 38.3%; Score 18; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WY 6
Db      4 WY 5

RESULT 3
Q9UK44 PRELIMINARY; PRT; 9 AA.
AC Q9UK44;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Signal transducer and activator of transcription 1 (Fragment).
GN STAT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Wong L.H., Sim H., Hatzinikisrou I., Ralph S.J.;
RT "STAT1 human genomic 5' intron 1.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF182314; AAF04559.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1212 MW; 86FFD72B0B4366C5 CRC64;

Query Match 38.3%; Score 18; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WY 6
Db      4 WY 5

RESULT 4
Q9UC36 PRELIMINARY; PRT; 9 AA.
AC Q9UC36;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shiohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin
RT from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
DR GO; GO:0003773; P:heat shock protein activity; NAS.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 38.3%; Score 18; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WY 6
Db      2 WY 3

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ID Q9UC36 PRELIMINARY; PRT; 9 AA.
AC Q9UC36;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shiohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin
RT from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
DR GO; GO:0003773; P:heat shock protein activity; NAS.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 38.3%; Score 18; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WY 6
Db      2 WY 3

RESULT 5
P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Kinin-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_TaxID=6978;
RP SEQUENCE, AND FUNCTION.
RX TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -1- FUNCTION: MYOTROPIC ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 31.9%; Score 15; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SW 5
Db      6 SW 7

RESULT 6
P82686 PRELIMINARY; PRT; 8 AA.
ID P82686

```

AC P82686;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinin-2 (PEA-K-2)
 OS Periplaneta americana (American cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta
 OK NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana."
 RL Regul. Pept. 71:199-205 (1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D58DDA CRC64;

Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 ||
 6 SW 7

RESULT 7
 P82687
 ID P82687 PRELIMINARY; PRT; 8 AA.
 AC P82687;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinin-3 (PEA-K-3)
 OS Periplaneta americana (American cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta
 OK NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana."
 RL Regul. Pept. 71:199-205 (1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 909 MW; DC6365B449DSA76A CRC64;

Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 ||
 6 SW 7

RESULT 8
 P82688
 ID P82688 PRELIMINARY; PRT; 8 AA.
 AC P82688;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinin-4 (PEA-K-4)
 OS Periplaneta americana (American cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta
 OK NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana."
 RL Regul. Pept. 71:199-205 (1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
 ||
 6 SW 7

RESULT 9
 P82689
 ID P82689 PRELIMINARY; PRT; 8 AA.
 AC P82689;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinin-5 (PEA-K-5)
 OS Periplaneta americana (American cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta
 OK NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana."
 RL Regul. Pept. 71:199-205 (1997).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- (MYOTROPIC ACTIVITY).
 CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 865 MW; C76365B449CDC775 CRC64;

Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SW 5
Db 6 SW 7

RESULT 10

Q8WGD7 ID Q8WGD7 PRELIMINARY; PRT; 8 AA.
AC Q8WGD7
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
OS Lomis hirta.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Lomoidea;
OC Lomidae; Lomis.
OX NCBI_TaxID=177234;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.B.; Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436035; AAL31611.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1038 MW; C5B5B9C733640321 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFS 4
Db 4 WLFS 7

RESULT 11

Q94V88 ID Q94V88 PRELIMINARY; PRT; 8 AA.
AC Q94V88
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus tristis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62052;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407533; AAL10151.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFS 4
Db 4 WLFS 7

RESULT 12

Q9T4Y2 ID Q9T4Y2 PRELIMINARY; PRT; 8 AA.
AC Q9T4Y2
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE COI gene product (Fragment).
OS Asterina pectinifera (Starfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89354669; PubMed=2766382;
RA Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA."
RL Curr. Genet. 15:193-206(1989).
DR EMBL; X16886; CAA34767.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1114 MW; F0C9D36415B736D6 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LFSWY 6
Db 3 LSRWF 7

RESULT 13

Q94VJ4 ID Q94VJ4 PRELIMINARY; PRT; 8 AA.
AC Q94VJ4
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus bengalensis nebulosis (Clouded monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169827;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407492; AAL10031.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; E8B5B9C733640056 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFS 4
Db 4 WLFS 7

```

RESULT 14
Q94V91
ID Q94V91 PRELIMINARY; PRT; 8 AA.
AC Q94V91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus timorensis (Timor monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62053;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407532; AAL10148.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPS 4
Db :|||
4 WLFS 7

RESULT 15
Q94VE4
ID Q94VE4 PRELIMINARY; PRT; 8 AA.
AC Q94VE4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus melinus (Quince monitor lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169846;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407511; AAL10087.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 31.9%; Score 15; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPS 4
Db :|||
4 WLFS 7

```

Search completed: March 18, 2004, 13:36:23
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:28:55 ; Search time 52 Seconds
(without alignments)
48.902 Million cell updates/sec

Title: US-09-920-480B-3

Perfect score: 47

Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	45	95.7	9	3 AAY84765	Aay84765 Antigenic
2	45	95.7	9	3 AAY84756	Aay84756 Antigenic
3	41	87.2	9	3 AAY84757	Aay84757 Antigenic
4	37	78.7	9	3 AAY84758	Aay84758 Antigenic
5	36	76.6	6	6 ABR47092	AbR47092 Staphyloc
6	35	74.5	9	3 AAY84771	Aay84771 Antigenic
7	35	74.5	9	3 AAY84761	Aay84761 Antigenic
8	34	72.3	6	6 ABR47091	AbR47091 Staphyloc
9	33	70.2	6	6 ABR47094	AbR47094 Staphyloc
10	33	70.2	6	6 ABR47052	AbR47052 Staphyloc
11	33	70.2	6	6 ABR47084	AbR47084 Staphyloc
12	32	68.1	6	6 ABR47068	AbR47068 Staphyloc
13	32	68.1	6	6 ABR47093	AbR47093 Staphyloc
14	32	68.1	6	6 ABR47076	AbR47076 Staphyloc
15	32	68.1	6	6 ABR45524	AbR45524 Staphyloc
16	31	66.0	6	6 ABR47051	AbR47051 Staphyloc
17	31	66.0	6	6 ABR46700	AbR46700 Staphyloc
18	31	66.0	6	6 ABR47096	AbR47096 Staphyloc
19	31	66.0	6	6 ABR47060	AbR47060 Staphyloc
20	31	66.0	6	6 ABR47083	AbR47083 Staphyloc
21	31	66.0	6	6 ABR45916	AbR45916 Staphyloc
22	31	66.0	8	5 ABJ11424	AbJ11424 Human 125
23	31	66.0	8	5 ABJ11390	AbJ11390 Human 125
24	31	66.0	8	5 AAO21946	Aao21946 HLA prima
25	31	66.0	8	5 ABJ16190	AbJ16190 Zinc tran

26	31	66.0	8	6 ABU72620	Novel pro
27	31	66.0	8	6 ABJ39326	Human Ieu
28	31	66.0	8	6 ABJ39290	Human Ieu
29	31	66.0	8	6 ABJ56971	184PIE2-r
30	31	66.0	8	6 ABJ56938	184PIE2-r
31	30	63.8	6	6 ABR47067	Staphyloc
32	30	63.8	6	6 ABR45523	Staphyloc
33	30	63.8	6	6 ABR47086	Staphyloc
34	30	63.8	6	6 ABR47075	Staphyloc
35	30	63.8	6	6 ABR47054	Staphyloc
36	30	63.8	9	3 AAY84759	Antigenic
37	29	61.7	6	5 AAU11829	Peptide 1
38	29	61.7	6	6 ABR45188	Staphyloc
39	29	61.7	6	6 ABR47053	Staphyloc
40	29	61.7	6	6 ABR45915	Staphyloc
41	29	61.7	6	6 ABR46308	Staphyloc
42	29	61.7	6	6 ABR47059	Staphyloc
43	29	61.7	6	6 ABR46699	Staphyloc
44	29	61.7	6	6 ABR45484	Staphyloc
45	29	61.7	6	6 ABR45526	Staphyloc

ALIGNMENTS

RESULT 1
AAY84765
ID AAY84765 standard; peptide; 9 AA.
XX
AC AAY84765;
XX
DT 08-AUG-2000 (first entry)
XX
DE Antigenic peptide epitope of gp100 polypeptide.
XX
KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
KW tumour antigen; vaccine; tumour cell; immune response; gp100.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "any amino acid"
FT
XX
PN WO200020457-A1.
XX
PD 13-APR-2000.
XX
PF 04-OCT-1999; 99WO-US023167.
XX
PR 05-OCT-1998; 98US-0103229P.
PR 05-JAN-1999; 99US-0114811P.
PR 11-FEB-1999; 99US-0120001P.
PR 11-FEB-1999; 99US-0120002P.
XX
PA (GENZ) GENZYME CORP.
XX
PI Nicolette CA;
XX
WPI; 2000-303749/26.
XX
PT New synthetic antigenic peptide epitopes related to insulin-like growth factor receptor, useful as vaccines against tumor cells expressing cell surface tumor antigen.
XX
PS Claim 12; Page 92; 116pp; English.
XX
CC AAY84763-69 represent synthetic antigenic peptide epitopes of gp100. The specification also describes synthetic epitopes of insulin-like growth factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class I or class II molecule with a higher affinity than the natural sequence.
CC The synthetic antigenic peptide epitopes may correspond to tumour antigens, and are therefore useful as vaccines against tumour cells

CC expressing cell surface tumour antigen. They are also useful in a variety
 CC of methods of modulating an immune response to the synthetic antigenic
 CC peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX Sequence 9 AA;

SQ

Query Match 95.7%; Score 45; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFSWYAXV 9
 Db |||||

1 FLFSWYAXV 9

RESULT 2

AA84756
 ID AAY84756 standard; peptide; 9 AA.

XX AC AAY84756;

XX DT 08-AUG-2000 (first entry)

XX DE Antigenic peptide epitope of insulin-like growth factor II receptor.

XX KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 XX KW tumour antigen; vaccine; tumour cell; immune response.

XX OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 8

FT /note= "any amino acid"

XX PN WO200020457-A1.

XX PD 13-APR-2000.

XX PF 04-OCT-1999; 99WO-US023167.

XX PR 05-OCT-1998; 98US-0103229P.

XX PR 05-JAN-1999; 99US-0114811P.

XX PR 11-FEB-1999; 99US-0120001P.

XX PR 11-FEB-1999; 99US-0120002P.

XX (GENZ) GENZYME CORP.

XX PA Nicolette CA;

XX PI WPI; 2000-303749/26.

XX DR New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.

XX PS Claim 1; Page 91; 116pp; English.

XX CC AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-
 CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
 CC a MHC class I or class II molecule with a higher affinity than the
 CC natural sequence. The synthetic antigenic peptide epitopes may correspond
 CC to tumour antigens, and are therefore useful as vaccines against tumour
 CC cells expressing cell surface tumour antigen. They are also useful in a
 CC variety of methods of modulating an immune response to the synthetic
 CC antigenic peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope

XX SQ Sequence 9 AA;

Query Match 95.7%; Score 45; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFSWYAXV 9
 Db |||||

1 FLFSWYAXV 9

RESULT 3

AA84757
 ID AAY84757 standard; peptide; 9 AA.

XX AC AAY84757;

XX DT 08-AUG-2000 (first entry)

XX DE Antigenic peptide epitope of insulin-like growth factor II receptor.

XX KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 XX KW tumour antigen; vaccine; tumour cell; immune response.

XX OS Synthetic.

XX PN WO200020457-A1.

XX PD 13-APR-2000.

XX PF 04-OCT-1999; 99WO-US023167.

XX PR 05-OCT-1998; 98US-0103229P.

XX PR 05-JAN-1999; 99US-0114811P.

XX PR 11-FEB-1999; 99US-0120001P.

XX PR 11-FEB-1999; 99US-0120002P.

XX (GENZ) GENZYME CORP.

XX PI Nicolette CA;

XX WPI; 2000-303749/26.

XX DR New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.

XX PS Claim 3; Page 91; 116pp; English.

XX CC AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-
 CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
 CC a MHC class I or class II molecule with a higher affinity than the
 CC natural sequence. The synthetic antigenic peptide epitopes may correspond
 CC to tumour antigens, and are therefore useful as vaccines against tumour
 CC cells expressing cell surface tumour antigen. They are also useful in a
 CC variety of methods of modulating an immune response to the synthetic
 CC antigenic peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope

XX SQ Sequence 9 AA;

Query Match 87.2%; Score 41; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLFSWYAXV 9

Db |||||

1 FLFSWYAXV 9

RESULT 4
 AAY84758
 ID AAY84758 standard; peptide; 9 AA.
 AC AAY84758;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Antigenic peptide epitope of insulin-like growth factor II receptor.
 XX
 KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 KW tumour antigen; vaccine; tumour cell; immune response.
 XX
 OS Synthetic.
 XX
 PN WO200020457-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 04-OCT-1999; 99WO-US023167.
 XX
 PR 05-OCT-1998; 98US-0103229P.
 PR 05-JAN-1999; 99US-0114811P.
 PR 11-FEB-1999; 99US-0120001P.
 PR 11-FEB-1999; 99US-0120002P.
 XX
 PA (GENZ) GENZYME CORP.
 XX
 PI Nicolette CA;
 FI
 DR WPI; 2000-303749/26.
 XX
 XX New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.
 XX
 PS Claim 4; Page 91; 116pp; English.
 XX
 CC AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-
 CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
 CC a MHC class I or class II molecule with a higher affinity than the
 CC natural sequence. The synthetic antigenic peptide epitopes may correspond
 CC to tumour antigens, and are therefore useful as vaccines against tumour
 CC cells expressing cell surface tumour antigen. They are also useful in a
 CC variety of methods of modulating an immune response to the synthetic
 CC antigenic peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX
 SQ Sequence 9 AA;
 Query Match 78.7%; Score 37; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 FLFSWYAXV 9
 Db 1 FLYSWWAIV 9
 RESULT 5
 ABR47092
 ID ABR47092 standard; peptide; 6 AA.
 AC ABR47092;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2282.
 XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; anti-inflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 PT Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 76.6%; Score 36; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLFSWY 6
 Db 1 FIFSWY 6
 RESULT 6
 AAY84771
 ID AAY84771 standard; peptide; 9 AA.
 AC AAY84771;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Antigenic peptide epitope of gp100 polypeptide.
 XX
 KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 KW tumour antigen; vaccine; tumour cell; immune response; gp100.
 XX
 OS Synthetic.
 XX
 PN WO200020457-A1.
 XX
 PD 13-APR-2000.

XX 04-OCT-1999; 99WO-US023167.
 XX 05-OCT-1998; 98US-0103229P.
 PR 05-JAN-1999; 99US-0114811P.
 PR 11-FEB-1999; 99US-0120001P.
 PR 11-FEB-1999; 99US-0120002P.
 XX (GENZ) GENZYME CORP.
 XX Nicolette CA;
 PI WPI; 2000-303749/26.
 DR New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.
 XX Disclosure; Page 110; 116pp; English.
 XX AAY84770-71 represent synthetic antigenic peptide epitopes of gpl00. The
 CC specification also describes synthetic epitopes of insulin-like growth
 CC factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class
 CC I or class II molecule with a higher affinity than the natural sequence.
 CC The synthetic antigenic peptide epitopes may correspond to tumour
 CC antigens, and are therefore useful as vaccines against tumour cells
 CC expressing cell surface tumour antigen. They are also useful in a variety
 CC of methods of modulating an immune response to the synthetic antigenic
 CC peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX Sequence 9 AA;
 SQ
 Query Match 74.5%; Score 35; DB 3; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 Db :|||||
 1 YLFSWY 6
 RESULT 7
 ID AAY84761
 XX AAY84761 standard; peptide; 9 AA.
 AC AAY84761;
 XX 08-AUG-2000 (first entry)
 DT Antigenic peptide epitope of insulin-like growth factor II receptor.
 DE Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 KW tumour antigen; vaccine; tumour cell; immune response.
 XX Synthetic.
 OS WO200020457-A1.
 XX 13-APR-2000.
 PD 04-OCT-1999; 99WO-US023167.
 XX 05-OCT-1998; 98US-0103229P.
 PR 05-JAN-1999; 99US-0114811P.
 PR 11-FEB-1999; 99US-0120001P.
 PR 11-FEB-1999; 99US-0120002P.
 XX (GENZ) GENZYME CORP.
 XX Nicolette CA;
 PI WPI; 2000-303749/26.
 DR New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.
 XX Disclosure; Page 110; 116pp; English.
 XX AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-
 CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
 CC a MHC class I or class II molecule with a higher affinity than the
 CC natural sequence. The synthetic antigenic peptide epitopes may correspond
 CC to tumour antigens, and are therefore useful as vaccines against tumour
 CC cells expressing cell surface tumour antigen. They are also useful in a
 CC variety of methods of modulating an immune response to the synthetic
 CC antigenic peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX Sequence 9 AA;
 SQ
 Query Match 74.5%; Score 35; DB 3; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 Db :|||||
 1 YLFSWY 6
 RESULT 8
 ID ABR47091
 XX ABR47091 standard; peptide; 6 AA.
 AC ABR47091;
 XX 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #2281.
 DE CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW synecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 PD 11-JUL-2001; 2001WO-EP008004.
 PF 11-JUL-2001; 2001WO-EP008004.
 PR 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 DR Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PI Nicolette CA;
 XX WPI; 2000-303749/26.
 XX New synthetic antigenic peptide epitopes related to insulin-like growth
 PT factor receptor, useful as vaccines against tumor cells expressing cell
 PT surface tumor antigen.
 XX Example 1; Page 85; 116pp; English.
 XX AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-
 CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
 CC a MHC class I or class II molecule with a higher affinity than the
 CC natural sequence. The synthetic antigenic peptide epitopes may correspond
 CC to tumour antigens, and are therefore useful as vaccines against tumour
 CC cells expressing cell surface tumour antigen. They are also useful in a
 CC variety of methods of modulating an immune response to the synthetic
 CC antigenic peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX Sequence 9 AA;
 SQ
 Query Match 74.5%; Score 35; DB 3; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 Db :|||||
 1 YLFSWY 6
 RESULT 8
 ID ABR47091
 XX ABR47091 standard; peptide; 6 AA.
 AC ABR47091;
 XX 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #2281.
 DE CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW synecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 PD 11-JUL-2001; 2001WO-EP008004.
 PF 11-JUL-2001; 2001WO-EP008004.
 PR 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 DR Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.
 XX Disclosure; Page 19; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 72.3%; Score 34; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 DB 1 FFESWY 6

RESULT 9
 ABR47094
 ID ABR47094 standard; peptide; 6 AA.
 AC ABR47094;
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2284.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 19; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 70.2%; Score 33; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 DB 1 FFESWY 6

RESULT 10
 ABR47052
 ID ABR47052 standard; peptide; 6 AA.
 AC ABR47052;
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2242.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 19; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 70.2%; Score 33; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFSWY 6
 |:|:|
 Db 1 FIFAWY 6

RESULT 11
 ABR47084
 ID ABR47084 standard; peptide; 6 AA.
 XX
 AC ABR47084;
 DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #2274.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX (JARI-) JARI PHARM BV.
 PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 PI WPI; 2003-256333/25.
 DR
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;

Query Match 70.2%; Score 33; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFSWY 6
 |:|:|
 Db 1 FIFAWY 6

RESULT 12
 ABR47068
 ID ABR47068 standard; peptide; 6 AA.
 XX
 AC ABR47068;
 DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #2258.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX (JARI-) JARI PHARM BV.
 PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 PI WPI; 2003-256333/25.
 DR
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;

Query Match 68.1%; Score 32; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLFSWY 6
 |:|:|
 Db 1 FIFDWY 6

RESULT 13
 ABR47093
 ID ABR47093 standard; peptide; 6 AA.
 XX
 AC ABR47093;
 XX

DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2283.
 DE
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 PD
 XX
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 PI
 DR WPI; 2003-256333/25.
 XX
 XX
 PT Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 68.1%; Score 32; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 | | | | |
 Db 1 FFSWY 6
 RESULT 14
 ABR47076
 ID ABR47076 standard; peptide; 6 AA.
 XX
 AC ABR47076;
 XX
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2266.
 DE
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW

KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 PD
 XX
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 PI
 DR WPI; 2003-256333/25.
 XX
 XX
 PT Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 68.1%; Score 32; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 | | | | |
 Db 1 FFEWY 6
 RESULT 15
 ABR45524
 ID ABR45524 standard; peptide; 6 AA.
 XX
 AC ABR45524;
 XX
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #714.
 DE
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.

XX	23-JAN-2003.
XX	
XX	11-JUL-2001; 2001WO-EP008004.
XX	
XX	11-JUL-2001; 2001WO-EP008004.
PR	(JARI-) JARI PHARM BV.
PA	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX	Van Strijp JAG;
PI	
XX	WPI; 2003-256333/25.
DR	
XX	
PT	Combination of peptides derived from chemotaxis inhibiting protein from
PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT	prophylaxis and treatment of inflammation, cardiovascular, skin and
PT	kidney diseases.
XX	
XX	Disclosure; Page 13; 89pp; English.
PS	
XX	
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC	Staphylococcus aureus. The peptide fragments are useful in the
CC	prophylaxis or treatment of diseases or disorders involving the C5a-
CC	receptor (C5ar) and/or formylated peptide receptor (FPR) or neutrophils,
CC	monocytes and endothelial cells or involving acute or chronic
CC	inflammation reactions. The diseases or disorders include cardiovascular
CC	diseases, disease of the central nervous system, gastrointestinal
CC	diseases, skin diseases, genitourinary diseases, joint diseases,
CC	respiratory diseases and HIV infection
XX	
SQ	Sequence 6 AA;
	Query Match 68.1%; Score 32; DB 6; Length 6;
	Best Local Similarity 66.7%; Pred. No. 1.4e+06;
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QY	1 FLFSWY 6
	: :
Db	1 FIFSWF 6